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GenCore version 5.1.6
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- protein search, using sw model OM protein October 14, 2003, 08:34:01; Search time 21.8636 Seconds (without alignments) 94.378 Million cell updates/sec Run on:

US-09-931-700-2 76 1 YGGHQIYQFTDKD 13 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

1107863 seqs, 158726573 residues Searched: 1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008

Listing first 45 summaries

Database :

SIDSI/gegdata/geneseq/geneseqp-embl/AA1988.DAT:*
/SIDSI/gegdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDSI/gegdata/geneseq/geneseqp-embl/AA1990.DAT:*
/SIDSI/gegdata/geneseq/geneseqp-embl/AA1991.DAT:*
/SIDSI/gegdata/geneseq/geneseqp-embl/AA1992.DAT:* /SIDS1/gcgdata/geneseg/genesegp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseg/genesegp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseg/genesegp-embl/AA2000.DAT:* /SIDS1/gogdata/geneseg/genesegp-emb1/AA2001.DAT:*/SIDS1/gogdata/geneseg/genesegp-emb1/AA2002.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:* /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*/SIDSI/gcgdata/geneseqpeneseqp-emb1/AA1984.DAT:*/SIDSI/gcgdata/geneseqg-emb2eap-emb1/AA1986.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:* /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1982.DAT:* A_Geneseq_19Jun03:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human preproadreno	Human preproadreno	Adrenomedullin pep	Human adrenomedull	Adrenomedullin pep	Rat adrenomedullin	Human adrenomedull	Adrenomedullin pep	Adrenomedullin pep
QI	AAW25159	AAW25160	AAB91762	AAE09827	AAB91768	AAE09819	AAB75110	AAB91759	AAB91765
B	18	18	22	22	22	22	22	22	22
% Query Match Length DB	13	31	31	31	40	20	52	52	52
% Query Match	100.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0
Score	92	57	57	57	57	57	57	57	57
Result No.	7	7	m	4	Ŋ	9	7	œ	6

	ರ		ĕ	Universal stress p	Linker peptide-adr	UspA(1-57)-(A)-(GS	USPA(1-56)-(DD)-(G	sal	l stress	UspA(1-84)-(A)-(GS	Universal stress p	Thioredoxin-(GSGSG	Human adrenomeduli	Rat adrenomedulin	Human adrenomedull	\vdash	a)	Porcine adrenomedu	r	Universal stress p	Adrenomedullin pep	Mouse ischaemic co	E	5.	13	Arabidopsis thalia		H. pylori cytoplas	Adrenomedullin pep	Lactococcus lactis		Human polypeptide,	٠	plexin-	Novel human diagno
AAE0981	ABP5	AAB7	AAB7511	ABJ186	AAB7	AAB751	AAB7			2 AAB75124		AAB7511			AAB6034			AAB4969					ABB6031		AAG3189		AAB3251				·	2 AAM93421	AA U000	ABB11	2 ABG21017
2 22																																			
52	iń	'n	Ŋ	in	Ö	12	12	12	12	14	14	17	18	18	18	18	18	18	18	20	Ŋ	18	86	75	16	77	51	244	m	18	51	71	183	184	187
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ALIGNMENTS

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Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone; skin; blood related; disease; type II diabetes; preeclampsia; neurotransmission regulation; allergy; mast cell degranulation; antibacterial; antifungal; wound repair.
                                                                                                                                                                                                                    /note= "residues 122-131 of preproadrenomedullin with Tyr-Gly-Gly attached at N-terminus"
                                                                                       Human preproadrenomedullin derived immunogen, PO71.
                                                                                                                                                                                            Location/Qualifiers
                     AAW25159 standard; peptide; 13 AA.
                                                                                                                                                                                                                                             13
/note= "amidated"
                                                                                                                                                                                                                                                                                                                            96WO-US13286.
                                                                                                                                                                                                                                                                                                                                                  96US-0013172.
                                                                   (first entry)
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                    12-MAR-1996;
18-AUG-1995;
                                                                                                                                                                                                                                                                               WO9707214-A1
                                                                                                                                                                                                                                                                                                                              16-AUG-1996;
                                                                                                                                                                          Homo sapiens
                                                                 08-DEC-1997
                                                                                                                                                                                                                                                                                                       27-FEB-1997.
                                           AAW25159;
                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                 Key
RESULT 1
            AAW25159
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WO200069900-A2.
 12-MAR-1996;
18-AUG-1995;
30-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB91762;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB91762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adrenomedullin (AM) peptides P070, P071, P072 and PAMP-20
were used for the production of anti-AM antibodies (Ab). P070 represents
preproAM amino acids (as) 34.41 with the sequence Tyr-Tyr attached at
the N-terminus, P071 represents preproAM as 122-131 with the sequence
Tyr-Gly-Gly attached at the N-terminus, P072 represents preproAM as
116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
for the prevention and/or treatment of cancers, e.g. adrenal, nervous
system, lung, colon, ovarian and breast cancer by inhibiting cell
growth. They are also useful for regulating insulin secretion and blood
glucose metabolism and therefore for treating and/or preventing diabetes
type II. They may be used for the diagnosis or treatment of conditions
relating to pregnancy e.g. preeclampsia. The Ab are also useful
areas of the central nervous system; (ii) lessening or inhibiting mast
cell degranulation and hence reducing the effects of an allergic
response; (iii) inhibiting or preventing bacterial and fungal growth (to
treat infection); (iv) facilitating wound healing; and (v) promoting
creat infection); (iv) facilitating wound healing; and (v) promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                     Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used in the diagnosis and treatment of type II diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone; skin; blood related; disease; type II diabetes; preeclampsia; neurotransmission regulation; allergy; mast cell degranulation; antibacterial; antifungal; wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "residues 116-146 of preproadrenomedullin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human preproadrenomedullin derived immunogen, PO72.
                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW25160 standard; peptide; 31 AA.
                                                                                                                                        Claim 1; Page 43; 106pp; English.
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                                             Hook W,
EJ, Walsh
95US-0002936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YGGHQIYQFTDKD 13
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                          Cuttitta F, Gray K,
Miller MJ, Unsworth
                                                                             WPI; 1997-165298/15.
                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09707214-A1.
30-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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Human adrenomedullin (AM) peptides P070, P071, P072 and PAMP-20
Were used for the production of anti-AM antibodies (Ab). P070 represents
preproAM amino acids (as) 34-41 with the sequence Tyr-Tyr attached at
the N-terminus, P071 represents preproAM as 122-131 with the sequence
Tyr-Gly-Gly attached at the N-terminus, P072 represents preproAM as
116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
for the prevention and/or treatment of cancers, e.g. adrenal, nervous
system, lung, colon, ovarian and breast cancer by inhibiting cell
system, lung, colon, ovarian and breast cancer by inhibiting cell
glucose metabolism and therefore for treating and/or preventing diabetes
type II. They may be used for the diagnosis or treatment of conditions
relating to pregnancy e.g. preeclampsia. The Ab are also useful
areas of the central nervous system; (ii) lessening or inhibiting mast
cell degranulation and hence reducing the effects of an allergic
response; (iii) inhibiting or preventing bacterial and fungal growth (to
treat infection); (iv) facilitating wound healing; and (v) promoting
organ and bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification; succinimidyl, maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                  Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 in the diagnosis and treatment of type II diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                Martinez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 57; DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred w. ive o; Mismatches
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                                                                                                                                                                         Macri C,
T;
                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 43; 106pp; English.
                                                                                                                                                                     Cuttitta F, Gray K, Hook W,
Miller MJ, Unsworth EJ, Walsh
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99US-0153406.
99US-0159783.
95US-0002514.
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Matches 10; Conservative
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RESULT 5
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                                                                                                                                                                            comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases. AMB90829 to AAB92441 represent preptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                  The present invention describes a modified therapeutic peptide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                           Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 31; 0.006; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                      Disclosure; Page 499-500; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 57; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09827 standard; peptide; 31 AA.
                           Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adrenomedullin peptide #2.
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Best Local Similarity 100.
Matches 10; Conservative
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(CONJ-) CONJUCHEM INC
                             Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-564216/63.
                                                      WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                     31 AA;
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                          Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE09827;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                           The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal medifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is human adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a modified therapeutic peptide (I)
Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                Score 57; DB 22; Length 31;
Pred. No. 0.006;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adrenomedullin peptide (AM) SEQ ID NO:944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB91768 standard; Peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Milner PG,
                                                        Claim 5; Column 6; 24pp; English.
                                                                                                                                                                                                                                                                                                                                              75.0%; £
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                      peptide receptor activity
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.7
                                                                                                                                                                                                                                                                                                                                                                                                                               4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HQIYQFIDKD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CONJ-) CONJUCHEM INC
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                                                                                                                                                                                                                                                                                                              31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200069900-A2.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001
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(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases. ARB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. on assays to identify and/or isolate CGRP receptors or with intact calls either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is rat adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; vasoactive peptide; calcitonin gene related peptide; CGRP;
CGRP-receptor identification; adrenomedullin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to antagonists of the vasoactive peptide
                                                                                                                                                                                                                                               Length 40;
                                                                                                                                                                                                                                      75.0%; Score 57; DB 22; Length 40 100.0%; Pred. No. 0.008; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09819 standard; peptide; 50 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0070504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat adrenomedullin peptide
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                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                        4 HQIYQFTDKD 13
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                                                                                                                                                                                                        40 AA;
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                                                                                                                                                                                                        Sequence
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The present invention describes a method (MI) for producing darenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                         Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adrenomedullin peptide (AM) SEQ ID NO:935.
                                                                                                                                                                                                                                                                                                                                                                                                                          Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 45; 75pp; Japanese.
                                                                                                                                                                              Human adrenomedullin (AM) protein.
                                                                                             AAB75110 standard; Protein; 52 AA.
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                                                                                                                                                                                                                                                                                                                                    10-OCT-2000; 2000WO-JP07023.
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                                                                                                                                                       (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                       Takimoto A, Mitsuda Y,
              26 HQIYQFTDKD 35
 HQIYQFIDKD 13
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N-PSDB; AAH19806.
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Gaps

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Indels

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DB 22; Length 50; 0.01;

75.0%; Score 57; DB 100.0%; Pred. No. 0.0 cive 0; Mismatches

Best Local Similarity 100. Matches 10; Conservative

Query Match

Milner PG, Holmes DL, Thibaudeau K;

2000WO-US13576.

99US-0153406. 99US-0134406

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us-09-931-700-2.rag

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Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                            (CONJ-) CONJUCHEM INC.
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                                                 WO200069900-A2
                                                                                                                                          17-MAY-2000;
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15-OCT-1999;
                                                                                            23-NOV-2000
    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (III) and a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not sultable as drug candidates as they require frequent odministration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half illeduces the action of peptidases to increase length of activity (half intracellular uptake and interference with physiological processes.

AAB90829 to AAB92441 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification; succinimidyl, maleimido group, amino, hydroxyl; thiol; hormone; growth factor; neurotransmitter.
Protection, endogenous therapeutic peptide; peptidase, conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a modified therapeutic peptide (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 57; DB 22; Length 52; 100.0%; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 498; 733pp; English.
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                                                                                                                                                                                                                                                                                             99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                        (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-112059/12.
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ses 10; Conserv
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                                                                                            Homo sapiens.
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15-0CT-1999;
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                                                                                                                  Synthetic.
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases in the activity are are interference with physiological processes. ARB90829 to AAB92441 represent invention.
Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CGRP-receptor identification; adrenomedullin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                Disclosure; Page 501; 733pp; English.
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adrenomedullin peptide #1.
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nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09818;
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hypotensive and vasodilator. The invention provides modified callitonin and related peptides, such as adrenomedullin, that have at least 70% identity to the native form but are modified such that the tendency of the peptide to aggregate is reduced. Preferred regions for modification include those for which the peptide is polymorphic amongst different species, which the peptide is polymorphic amongst different species, which increase the propensity of the peptide to form local interactions of the alpha-helical type, or which reduce the number of hydrophobic residues or increase the net charge of the peptide. When aggregation is reduced or prevented, lower doses of the drug can be used. Side-effects and undesired responses are minimised by retaining high sequence identity to the human peptide.
              present sequence is that of human adrenomedullin, a potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 46; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                   AAB75111 standard; Protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0294147.
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                 4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                       28 HOIYOFTDKD 37
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AA;
                                                                                                                                                                                        52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH19807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-2001
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                            AAB75111;
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                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                      AAB7511.
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                                                                                                                                                                                  calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. cells either in vitro or isolate CGRP receptors or with intact binding to its receptor. The present sequence is human adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified human calcitonin peptide having reduced aggregation, useful for the treatment of Paget's disease, hypercalcemia and/or
                                                                                                          Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                         The invention relates to antagonists of the vasoactive peptide
                                                                                                                                                                                                                                                                                                                                     DB 22; Length 52; 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adrenomedullin, human; protein engineering; solubility; aggregation; hypotensive; vasodilator; cyclic.
                                                                                                                                                                                                                                                                                                                                                            .0
                                                                                                                                                                                                                                                                                                                                   75.0%; Score 57; DB 100.0%; Pred. No. 0.0
                                                                                                                                               Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
16..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP55104 standard; Peptide; 52 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 21; 35pp; English.
           98US-0070504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                          peptide receptor activity
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                    (DYCR-) UNIV CREIGHTON.
                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                   Human adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dobson CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-046916/04.
                                                                                                                                                                                                                                                                                                                                                                                     4 HQIYQFTDKD
                                                                                   WPI; 2001-564216/63
                                                          Saha S,
                                                                                                                                                                                                                                                                                                            52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis
           30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2002
                                                          Smith DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP55104;
                                                                                                                                                                                                                                                                                                             Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                    Gaps
                                                                                                                        ö
                              Score 57; DB 24; Length 52; Pred. No. 0.011;
                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
75.0%; Score
100.0%; Pred. No. v.
0; Mismatches
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Claim 4; Page 30; 49pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                 04-APR-2002; 2002WO-JP03374.
                                                                                                                                                                                                                              10-APR-2001; 2001JP-0111088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
          27-FEB-2003 (first entry)
                                                                                                                                                                                                                                                         (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOIYOFIDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOIYOFTDKD
                                                                                                                                                                                                                                                                                                                    WPI; 2003-067581/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 AA;
                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABT14525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200127310-A1.
                                                                                                                                         WO200283907-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                       by cleavage
                                                                                                                                                                       24-OCT-2002.
                                                                                                                                                                                                                                                                                          Mitsuda Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75113;
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                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                     Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 22; Length 55, Pred, No. 0.011;
            Length 53;
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                             Glycine extended adrenomedullin (AM-gly) protein.
            DB 22;
0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%; Scor.
100.0%; Pred. No. v...
0; Mismatches
            Score 57; DB 2
Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 47; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABJ18665 standard; Protein; 53 AA.
                                                                                                                                                                         AAB75112 standard; Protein; 53 AA.
    75.0%; Scc.
100.0%; Pre
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCI-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0294147.
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
               Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 HQIYQFTDKD 13
                                                                                      4 HQIYQFIDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-282044/29.
N-PSDB; AAH19808.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AA;
                                                                                                                                                                                                                                                                                                                                                                             WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-0CT-1999;
                                                                                                                                                                                                                                 31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-2001
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                     AAB75112;
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Homo

RESULT 13

δŏ qq AAB753

ABJ18665;

RESULT 14

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ABJ18665

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The invention comprises a novel fusion peptide which contains an Escherichia coli universal stress protein (USpA), a linker peptide and a target peptide. The fusion protein is cleavable by a protease. The fusion peptide of the invention is useful for the efficient large scale production of peptides. The present amino acid sequence represents a protein that was used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                   Fusion peptide; universal stress peptide; UspA; linker peptide; large scale peptide production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linker peptide-adrenomedullin (AM) precursor protein.
Universal stress protein A (uspA)-related protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 57; DB 24;
100.0%; Pred. No. 0.011;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75113 standard; Protein; 62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0294147
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(SHIO) SHIONOGI & CO LID.

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The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host \,\cdot\,
                                                             Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                   Claim 20; Page 48; 75pp; Japanese.
                                                                                                  WPI; 2001-282044/29.
N-PSDB; AAH19809.
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Query Match 75.0%; Score 57; DB 22; Length 62; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels 4 HQIYQFIDKD 13 δž Q

62 AA;

Seguence

0

Gaps 0;

Search completed: October 14, 2003, 08:38:46 Job time: 22.8636 secs

us-09-931-700-2.rai

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October 14, 2003, 08:37:31; Search time 8.56818 Seconds (without alignments) 64.196 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                            328717 seqs, 42310858 residues
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Issued_Patents_AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 15, Appl	1,	7	e,	4,	5, 2	23,	'n	Sequence 14, Appl	9	ģ	Sequence 8, Appli	11,	15,	7, 7	14	Sequence 1, Appli	'n	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	'n	Sequence 3, Appli	17, A	Sequence 116, App
SUMMAKLES	ID	US-09-011-922A-2	US-09-280-501-15	US-09-280-501-1	US-09-280-501-2	US-09-280-501-3	US-09-280-501-4	US-09-280-501-5	US-09-070-504-23	US-09-011-922A-3	US-09-011-922A-14	US-09-280-501-9	US-09-280-501-6	US-09-280-501-8	US-09-280-501-11	US-09-070-504-15	-60	US-09-070-504-14	US-08-233-389C-1	US-08-801-863-1	US-08-486-596A-1	US-09-004-713-1	US-08-233-389C-3	US-08-801-863-3	US-08-486-596A-3	-00-004-	280-501	US-09-266-965-116
	DB	4	4	4	4	4	4	4	m	4	4	4	4	4	4	٣	4	æ	Н	7	7	7	Н	~	7	~	4	4
	Length	13	13	26	27	28	29	30	31	31	31	31	38	40	40	20	20	52	185	185	185	185	188	188	188	188	23	514
æ	Query Match	100.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	57.9	57.9
	Score	92	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	44	44
	Result No.	П	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	1.9	20	21	22	23	24	25	26	27

	259	Sequence 6, Appli Sequence 2, Appli	6073	Sequence 75, Appl Sequence 53, Appl	Sequence 12, Appl		Sequence 35/3, Ap Sequence 24398, A	Sequence 2, Appli	Sequence 118, App	Sequence 2, Appli	Sequence 4347, Ap
US-09-252-991A-19737 US-09-634-238-241	US-09-252-991A-25900 US-09-252-991A-21838	US-U9-368-169-8 US-09-306-881-2 HE-00-107-5328-5662	US-09-107-532A-6073	US-09-599-360B-75 US-08-851-567B-53	US-08-851-567B-12	US-07-998-289B-4	US-U9-1U/-532A-35/5 US-09-252-991A-24398	US-09-333-423-2	US-09-266-965-118	US-09-581-831-2	US-09-134-001C-4347
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264	433	374	418	302 1844	2504	196	291	347	470	484	514
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41	4 6 6 0 9 6	38.59	38	37	37	36	9 B 00 B	36	36	36	36
2 2 8	30 31 31		# 45 12	36	38	σe.	4 4	42	43	44	45

ALIGNMENTS

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Sequence 2, Application US/09011922A

Patent No. 6320022
GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo; Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macril, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
WUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-42020S3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAS: (212) 758-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: LESLIE A. SETUNIAN
                                                                                                                                                                                                                                                                                                                                                                                 MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                        : 345 Park Avenue
New York
                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
US-09-011-922A-2
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Page

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SEQ ID NO 3
LENGIH: 28
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                       Query Match
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GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reld, Ian Reginald
APPLICANT: Cornish, Jillian
ITILE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
ITILE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08997-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT APPLICATION NUMBER: 08/034,562
PRIOR FILING DATE: 1996-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Coorish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: 08/09/280,501
CURRENT FILING DATE: 1990-03-30
PRIOR FILING DATE: 1996-04-18
                                                                                                                                                                                                  Query Match 100.0%; Score 76; DB 4; Length 13; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                           ; NAME/KEY: P071
; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09280501
Patent No. 6440421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-280-501-1; Sequence 1, Application US/09280501; Sequence 1. Application US/09280501; Patent No. 6440421; GENERAL INFORMATION:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  1 YGGHQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                        1 YGGHQIYQFTDKD 13
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                                            : peptide
No
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CORGANISM: Homo sapiens
US-09-280-501-1
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US-09-280-501-15
                                      TOPOLOGY: lin
MOLECULE TYPE: N
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US-09-280-501-15
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LENGTH: 26
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LENGIH: 13
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APPLICANT: Cooper, Garth James Smith
APPLICANT: Cooper, Garth James Smith
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
FILE REFERENCE: 08908 ADERBOWEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08908 TOSEON
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03330
PRIOR FILING DATE: 1996-04-18
75.0%; Score 57; DB 4; Length 26; 100.0%; Pred. No. 0.0033; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 57; DB 4; Length 27; 100.0%; Pred. No. 0.0034; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 57; DB 4; Length 28; 100.0%; Pred. No. 0.0035; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. mc.
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 27
                                                                                                                                                                           ; Sequence 2, Application US/09280501; Patent No. 6440421
                Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
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                                                                4 HQIYQFTDKD 13
                                                                                                2 HQIYQFIDKD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Homo sapiens
US-09-280-501-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                              RESULT 4
US-09-280-501-2
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APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo; Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
APPLICANT: Raren; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 57; DB 3; Length 31; 100.0%; Pred. No. 0.0039; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/070,504 FILING DATE: 30-APR-1998
  TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGI
TITLE OF INVENTION: SUPERFAMILY AND METHODS OI
WINDER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6568474th Fourth Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCCOIMACK, MYTA H
REGISTRATION NUMBER: 36,602
REGISTRATION NUMBER: 36,602
TELEPRENCE_POCKET NUMBER: 180.00020101
TELEPHONE: 612/305-1220
TELEPHONE: 612/305-1228
INFORMATION FOR SEQ ID NO: 23:
INFORMATION FOR SEQ ID NO: 23:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09011922A; Patent No. 6320022; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                    COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-PARTMANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                         ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 HQIYQFTDKD 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30
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                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
ITILE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
ITILE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                    APPLICANT: Cooper, Garth James Smith
APPLICANT: Cooper, Garth Jallah
APPLICANT: Cornish, Jillian
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREAPMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 4
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%; Score 57; DB 4; Length 29; 100.0%; Pred. No. 0.0037; tive 0; Mismatches 0; Indels
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Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09280501
; Patent No. 6440421
                                                                     Sequence 4, Application US/09280501
Patent No. 6440421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.0%
Best Local Similarity 100.0
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-280-501-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-070-504-23
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US-09-280-501-5
                            RESULT 6
US-09-280-501-4
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LENGIH: 30
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APPLICATION NUMBER: US/60/002,936
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Matches 10; Conserv
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Best Local Similarity
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APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Marci, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; DB 4; Length 31; 100.0%; Pred. No. 0.0039; Live 0; Mismatches 0; Indels
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                                                              PRICA AND CALE.

PRICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
FILING DATE: 31-Aug-1995
PRICATION NUMBER: US/60/013,172
PRICA APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
APPLICATION NUMBER: PCT/US96/13286
APPLICATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 30.363
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           2026-4202US3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , NAME/KEY: P072
; OTHER IMFORMATION: PreproAM(116-146)
US-09-011-922A-3
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ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09011922A Patent No. 6320022
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MEDIWM TYPE: Floppy Disk
COMPUTER: IMP PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 345 Park Avenue
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amino acid
GY: linear
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Best Local Similarity 100.
Matches 10; Conservative
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ZIP: 10154-0053
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US-09-011-922A-14
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US-09-280-501-9

Sequence 9, Application US/09280501

Patent No. 6440421

GENERAL INFORMATION:

APPLICANT: Cooper, Garth James Smith

APPLICANT: Cornish, Jillian

TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH

TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS

FILE REFERENCE: 08997-005001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic homolog of two-thirds of the intact AM peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; DB 4; Length 31; 100.0%; Pred. No. 0.0039; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 57; DB 4; Length 31; 100.0%; Pred. No. 0.0039; Arive 0; Mismatches 0; Indels
                                                                                                                                                                                  NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 756-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09280501; Patent No. 6440421; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
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; ORGANISM: Homo sapiens
US-09-280-501-9
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Gaps

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                                                                                                                                                                                                          75.0%; Score 57; DB 4; Length 40; 100.0%; Pred. No. 0.0051; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%; Score 57; DB 3; Length 50; 100.0%; Pred. No. 0.0065; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180.00020101
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 40
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APPLICATION NUMBER: US/09/070,504
FILLING DATE: 30-APR-1998
CLASSIFTCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Sha, Shankar
APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 612/365-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                          Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-09-070-504-15
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                                                                                                                                                                                                                                                                                                        4 HQIYQFTDKD 13
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                                                                                                                                           ORGANISM: Homo sapiens
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US-09-070-504-15
                                                                                                                                                                 US-09-280-501-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                   TYPE: PRT
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Sequence 8, Application US/09280501

Sequence 8, Application US/09280501

Sequence 8, Application US/09280501

Sequence 8, Application

Sequence 8, Application

APPLICANT: Cooper, Carth James Smith

APPLICANT: Reid, Ian Reginald

APPLICANT: Reid, Ian Reginald

APPLICANT: Cornish, Jillian

TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS

FILE REFERENCE: 0898-005001

CURRENT APPLICATION NUMBER: US/09/280,501

CURRENT FILING DATE: 1999-03-30

PRIOR FILING DATE: 1996-04-18

NUMBER OF SEQ ID NOS: ID NOS: ID NOS: ID NOS: IN NUMBER: EastSEQ for Windows Version 4.0
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APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
TITLE OF INVENTION: 19987-005001
CURRENT APPLICATION UNDRER: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
IITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
IITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 57; DB 4; Length 40; 100.0%; Pred. No. 0.0051; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 57; DB 4; Length 38; 100.0%; Pred. No. 0.0049; tive 0; Mismatches 0; Indels
                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/280,501 CURRENT FILING DATE: 1999-03-30 PRIOR APPLICATION NUMBER: 08/634,562 PRIOR FILING DATE: 1996-04-18
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09280501
Patent No. 6440421
                                                                                                                 FILE REFERENCE: 08987-005001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-280-501-11
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LENGTH: 40
                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGIH: 38
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 14, 2003, 08:40:27; Search time 26 Seconds (without alignments) 80.564 Million cell updates/sec Run on:

US-09-931-700-2 76 Title:

1 YGGHQIYQFTDKD 13 Perfect score:

BLOSUM62 Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

600653 seqs, 161128416 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

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5: cgn2_6/ptodata/Z/pubpaa/US09_PUBCOMB.pep:*
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6: cgn2_6/ptodata/Z/pubpaa/US10C_PUBCOMB.pep:*
7: cgn2_6/ptodata/Z/pubpaa/US10C_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli		Sequence 14, Appl	Sequence 23, Appl	Sequence 15, Appl	Sequence 14, Appl	Sequence 2, Appli	Sequence 116, App	Sequence 116, App	Sequence 2, Appli	Sequence 5230, Ap	Sequence 306, App	Sequence 5238, Ap	Sequence 6765, Ap	Sequence 66, Appl
SUMMARIES	TD	US-09-931-700-2	US-09-931-700-3	US-09-931-700-14	US-09-813-345-23	US-09-813-345-15	US-09-813-345-14	US-10-197-954-2	US-09-953-348-116	US-10-267-255-116	US-10-027-000-2	US-08-781-986A-5230	US-09-801-368-306	US-09-738-626-5238	US-09-738-626-6765	US-09-895-298-66
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	Query Match Length DB	13	31	31	31	20	52	52	514	514	833	519	1356	325	161	302
dР	Query Match	100.0	75.0	75.0	75.0	75.0	75.0	75.0	57.9	57.9	57.9	53.9	51.3	50.0	48.7	48.7
	Score	16	57	57	57	57	57	57	44	44	44	41	39	38	37	37
	Result No.	1	71	e	4	Ŋ	9	7	8	6	10	11	12	13	14	15

Sequence 120, Applisequence 2, Applisequence 3, Applisequence 12, Applisequence 12, Applisequence 1062, Applisequence 1062, Applisequence 1075, Applisequence 1075, Applisequence 1033, Applisequence 12332, Applisequence 12332, Applisequence 12470, Applisequence 6, Applisequence	و و
111 US-09-895-298-120 12 US-10-254-074-2 13 US-10-254-074-2 14 US-10-242-056-13 15 US-10-242-056-12 10 US-09-917-514A-8 10 US-09-955-999-71 10 US-09-955-999-71 10 US-09-955-999-71 11 US-09-955-999-71 12 US-10-955-999-71 13 US-09-955-999-71 14 US-09-955-999-71 15 US-09-915-242-1889 16 US-09-915-242-1870-9 17 US-10-140-018-6 18 US-10-140-018-6 19 US-10-140-018-6 11 US-10-140-018-6 12 US-10-140-018-6 13 US-10-140-018-6 14 US-10-140-018-6 15 US-10-140-018-6 17 US-10-140-018-6 18 US-10-141-098-6	US-10-142-42
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м о о о о о о о о о о о о о о о о о о о	36
HHHHUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	45

ALIGNMENTS

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APPLICANT: MATILER, ALENDO
APPLICANT: MILLER, MAE JEAN
APPLICANT: WILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KAREN
APPLICANT: GREY, KAREN
APPLICANT: GREY, KAREN
TITLE OF INVEWTION: FUNCTIONAL FORGLEY
TITLE OF INVEWTION: Physiology
TITLE OF INVEWTION: Physiology
TITLE OF INVEWTION: Physiology
FILE REFERENCE: 2026-4202084
CURRENT APPLICATION NUMBER: US/09/931,700
FILE REPERENCE: 2026-4202084
CURRENT FILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1996-03-16
PRIOR FILING DATE: 1996-03-16
PRIOR FILING DATE: 1996-03-16
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Peptide, OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)
Sequence 2, Application US/09931700 Patent No. US20020055615A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                          APPLICANT: CUTTITTA, FRANK APPLICANT: MARTINEZ, ALFREDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 2
LENGTH: 13
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us-09-931-700-2.rapb

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SEQ ID NO 14
LENGTH: 31
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APPLICANT: MALLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: GREY, KAREN
APPLICANT: GREY, KAREN
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Gene-Felated Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
FILE REPERENCE: 2056-4202054
CURRENT APLICATION NUMBER: US/09/931,700
CURRENT APLICATION NUMBER: 105(09/931,700
CURRENT FILING DATE: 1996-02-17
PRIOR APPLICATION NUMBER: US/00/013,172
PRIOR FILING DATE: 1966-08-16
PRIOR FILING DATE: 1966-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1995-08-16
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
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                                             Length 13;
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                                                                                   Indels
                                         100.0%; Score 76; DB 9; L ilarity 100.0%; Pred. No. 1.6e-06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09931700 Patent No. US20020055615A1
                                                                                                                                                                                                                                                                    Sequence 3, Application US/09931700
Parent No. US20020055515A1
GENERAL INFORMATION:
APPLICANT: CUTIITTA, FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNSWORTH, EDWARD J.
HOOK, WILLIAM
WALSH, THOMAS
GREY, KAREN
MACRI, CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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MILLER, MAE JEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                        1 YGGHQIYQFTDKD 13
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Best Local Similarity 100.
Matches 10, Conservative
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APPLICANT: CUTTITIA, FRANK
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                                       Query Match
Best Local Similarity
Matches 13; Conserv
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US-09-931-700-14
                                                                                                                                                                                                                               SULT 2
-09-931-700-3
US-09-931-700-2
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
FILE REPERBENCE: 2026-4202054
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US/011,922
PRIOR PELICATION NUMBER: US/0/011,922
PRIOR PELICATION NUMBER: US/0/013,172
PRIOR PELICATION NUMBER: US/60/013,172
PRIOR PELICATION NUMBER: US/60/013,172
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-12
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
SOUTHWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFFLLENS. Shankar
Saha, Shankar
Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.0%; Score 57; DB 9; Length 31; Best Local Similarity 100.0%; Pred. No. 0.0065; Matches 10; Conservative 0; Mismatches 0; Indels
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ADDRESSE: Mucting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814A1th Fourth Street
CIIY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <u >Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MCCOTMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
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TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-813-345-23
; Sequence 23, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 23:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 14, Application US/09813345
                     Patent No. US20020068814A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; DB 9; Length 50; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels
                                                                                                                                                                                    Length 31;
                                                                                                                                                                                  Query Match 75.0%; Score 57; DB 9; Length 31; Best Local Similarity 100.0%; Pred. No. 0.0065; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814Alth Fourth Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMPUTER: TBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,602
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09813345 Patent No. US20020068814A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MCCOIMACK, Myra H
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
                       LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, Derek D.
                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saha, Shankar
Abel, Peter W.
SEQUENCE CHARACTERISTICS:
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Best Local Similarity luv..
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                           HQIYQFTDKD 35
                                                                                                                                                                                                                                                                   4 HQIYQFTDKD 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           US-09-813-345-15
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US-09-813-345-14

RESULT 6

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Sequence 2, Application US/10197954
Publication No. US20030119021A1
GENERAL INFORMATION:
APPLICAMY: Kister, Hubert
APPLICAMY: Siddidi, Subalb
APPLICAMY: Siddidi, Subalb
APPLICAMY: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: Cappositions
TITLE OF INVENTION: Cappositions
FILE REFRENCE: 24743-2205
CURRENT APPLICATION NUMBER: US/10/197,954
CURRENT PELING DATE: 2002-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-08-21
PRIOR PILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: Smith, Derek D.
Saha, Shankar
Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%; Score 57; DB 9; Length 52; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                 ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. US20020068814Alth Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: CLASSIFICATION: CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCCOIMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 14:
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                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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Matches 10; Conserv
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us-09-931-700-2.rapb

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LENGTH: 833
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                                                                                                                       Score 57; DB 15; Length 52;
Pred. No. 0.011;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sherman, David. H
APPLICANT: Sherman, David. H
APPLICANT: Aaco, Yingqing
APPLICANT: Varcoglu, Mustafa
APPLICANT: Tarcoglu, Mustafa
APPLICANT: Sheldon, Paul
TITLE OF INVENITON: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
FILE REFERENCE: 600.530US1
CURRENT APPLICATION NUMBER: US/09/953,348
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 097/266965
PRIOR FILING DATE: 1099-03-12
PRIOR FILING DATE: 1099-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Machinal, E.
APPLICANT: Machinal, E.
APPLICANT: Varoglu, M
APPLICANT: He, M
APPLICANT: He, M
APPLICANT: Beldon, P
ITILE OF INVENTION: Mitomycin biosynthetic gene cluster: FILE REFERENCE: 600.456019
FILE REFERENCE: 600.456019
FRIOR APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 1999-03-12
FRIOR FILING DATE: 1999-03-12
FRIOR FILING DATE: 1996-08-19
FRIOR FILING DATE: 1994-10-06
FRIOR APPLICATION NUMBER: PCI/US94/11279
FRIOR PELICATION NUMBER: PCI/US94/11279
FRIOR PELICATION NUMBER: US 08/133,963
FRIOR FILING DATE: 1994-10-06
FRIOR APPLICATION NUMBER: US 08/133,963
FRIOR FILING DATE: 1993-10-07
                                                                                                          75.0%; Scc..
100.0%; Pred. No. v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 153
SOFTHRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                    ; Sequence 116, Application US/09953348; Publication No. US20030134398A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 116, Application US/10267255; Publication No. US20030124689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Streptomyces lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 80.0
Matches 8; Conservative
                                                                                                                         Query Match
Best Local Similarity 100,
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GGHGIYQFYD 75
                                                                                                                                                                                                                                 2 GGHQIYQFTD 11
                                                                                                                                                                                                           4 HQIYQFIDKD 13
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                                                         ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                 US-10-197-954-2
SEQ ID NO 2
LENGIH: 52
                                       TYPE: PRT
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Sequence 5230, Application US/08781986A

Publication No. US20030054436A1

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Publication No. US20030119006A1

GENERAL INRORMATION:

APPLICANT: Goedegebuur, Frits

APPLICANT: Ward, Michael

APPLICANT: Yao, Jian

TITLE OF INVENTION: BGL4 Beta-Glucosidase and Nucleic Acids

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: GC66

CURRENT APPLICATION NUMBER: US/10/027,000

CURRENT PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 15; Length 833;
Pred. No. 34;
3; Mismatches 3; Indels
                                                                                                                                                  Score 44; DB 15; Length 514;
Pred. No. 21;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 116 LENGIH: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/781,986A
                                                                ; TYPE: PRT; ORGANISM: Streptomyces lavendulae US-10-267-255-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.9%;
53.8%;
                                                                                                                                                      57.9%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | :: | :| |||
682 YVGYRYYEFADKD 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YGGHQIYQFTDKD 13
                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.9
Best Local Similarity 53.8
Matches 7; Conservative
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      2 GGHQIYQFTD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-781-986A-5230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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Score 37; DB 10; Length 161;
Pred. No. 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 10;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                    FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL POLYNUCLECTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DAIE: 2000-12-18
                                                                                                                                                      APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6765
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6765, Application US/09738626
Publication No. US20020197605A1
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6775
LENGTH: 161
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              HIROSHI
                                                                                 YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANDO, SEIKO
HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCHIAI, KEIKO
YOKOI, HARUHIKO
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SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 50...
6; Conservative
                                                  HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGHQIYQFTDKD 13
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13 GGPEVLEFTDID 24
                                                                    OCHIAI, KEIKO
                                                                                                                                         IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OZAKI, AKIO
              MIZOGUCHI, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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US-09-738-626-6765
                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5238
LENGTH: 325
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APPLICANT:
APPLICANT:
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                                                                  APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
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                                                                                                                                                                                                                                                                                 Score 41; DB 8; Length 519;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
             NAME: Benson, Bob:
REGISTRATION NUMBER: 90,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION: TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5230: SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/160,587 PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5238, Application US/09738626
; Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 306, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccharomyces cerevisiae US-09-801-368-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 306
LENGTH: 1356
                                                                                                                                                                                                                                                                               53.9%;
66.7%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.55
Local 5; Conservative
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66./r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cali, Brian
Hecht, Peter
Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                         454 GGROIGOFSSKD 465
                                                                                                                                                                                                                                                                                                                                                        2 GGHQIYQFTDKD 13
                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salama, Sofie
Sherman, Amir
                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-781-986A-5230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 HEVYEFTD 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 HQIYQFTD 11
                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-801-368-306
                                                                                                                                                                                                                TOPOLOGY:
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APPLICANT:
APPLICANT:
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Gaps

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1 LOCATION: (237)

2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-895-298-66
    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels
    3; Indels
                                                                                                                                    RESULT 15
US-09-895-298-66

Sequence 66. Application US/09895298

Publication No. US20030078405A1

CENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 41

CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT APPLICATION NUMBER: O9/591,16

PRIOR FILING DATE: 2001-07-02

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 231

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 66

LENGTH: 100 66
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 14, 2003, 08:53:16 Job time : 26 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | |:| ||::
| 176 YPGLQVYTFTER 187
7; Conservative
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                                                            ||:| |||||
62 GHRISNTTDKD 72
                                      3 GHQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 14, 2003, 08:36:56; Search time 7.38636 Seconds (without alignments) 169.257 Million cell updates/sec Run on:

US-09-931-700-2 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 YGGHQIYQFIDKD 13

Sequence:

283308 segs, 96168682 residues Searched: 283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR 76:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
н	57	ın	185	7	JN0684	adrenomedullin pre
7	57	75.0	185	ď	JN0766	in
m	57	75.0	188	7	S41600	
4	51	67.1	643	7	876069	hypothetical prote
Ŋ	45		776	~	T02702	
9	44	57.9	2231	N	D71870	н
7	42		280	7	H70089	_
σο	42		324	~	A87544	ч
თ	42	55.3	350	~	T21106	hypothetical prote
10	42		563	7	T09378	hypothetical prote
11	41		185	7	C86705	а
12	41	-	467	~	T21690	Н
13	41	53.9	514	7	D89775	_
14	40	52.6	146	ď	G83445	conserved hypothet
15	40	52.6	260	ď	H71979	probable type II r
16	40	52.6	275	7	T32005	hypothetical prote
17		52.0	909	N	T40556	
18	39	51.3	176	7	B35697	_
19		51.3	310	~	98669н	hypothetical prote
20		51.3	444	Н	E69130	histidine-tRNA lig
21	39	51.3	705	7	JX0194	prolyl oligopeptid
22	39	51.3	1356	7	S51389	ROM2 protein - yea
23	38.5	50.7	322	7	T22410	pī
24	38	50.0	165	7	F69819	conserved hypothet
25	38	50.0	254	7	B70860	probable enoyl-CoA
26	38		257	7	AH0859	periplasmic fimbri
27	38	50.0	264	7	T23866	hypothetical prote
28	38	50.0	387	7	340	
29	38	50.0	391	7	H89859	hypothetical prote

F)1-21/Domain: Signal sequence #status predicted <SIG>
F)22-14/Domain: Signal sequence #status predicted <PBU>
F)22-14/Domain: proadrenomedullin #status predicted <PBU>
F)22-14/Domain: proadrenomedullin #status verpenimal 20 peptide #status predicted <PAP>
F)22-14/Fyroduct: adrenomedullin #status experimental <MAT>
F)147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F)147-185/Domain: amidated carboxyl end (Arg) (amide in mature form from following F)110-115/Disulfide bonds: #status experimental
F)146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

A;Map position: 11pter-11qter A;Introns: 33/2; 83/2 C;Keywords: amidated carboxyl end; blood pressure control; hormone

ö

0; Gaps

75.0%; Score 57; DB 2; Length 185; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels

Query Match 75.0% Best Local Similarity 100.4 Matches 10; Conservative

protein kinase, ca	protein kinase, ca	pectate lyase rela	pepT protein - Sta	ABC transporter, A	hypothetical prote	hypothetical prote	dextranase - Strep	alpha-amylase (EC	hypothetical prote	probable lipoprote	rfbT protein VC025	oxidoreductase ypi	sugar phosphate nu	imidazoleglycerol-	hypothetical prote
817759	T14335	A96999	S58356	A95167	H98032	E84534	T30291	JS0101	T26838	AG0539	HB2344	B86817	F90507	E82238	T29832
7	N	~	7	~	7	ď	~	~	~	7	~	~	7	a	01
425	532	564	571	286	586	952	1337	269	105	164	227	250	253	257	285
50.0	20.0	50.0	50.0	50.0	50.0	50.0	50.0	49.3	48.7	48.7	48.7	48.7	48.7	48.7	48.7
38	38	38	38	38	38	38	38	37.5	37	37	37	37	37	37	37
30	31	32	33	34	35	36	37	38	6E	40	41	42	43	77	45

ALIGNMENTS

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A.Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 22-41 < KII2>
B;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy A;Reference number: JN0476; MUID:93249425; PMID:8387282
A;Molecule type: protein
A;Residues: 95-146 < KI3>
                                                                                                                                                                                                                                                                                                                                                                                                          A Rolecule type: DNA
A Residues: 1-185 <18517
A Residues: 1-185 <18517
A Residues: 1-186 <18517
A Residues: 1-186 <18517
A Experimental source: phecohromocytoma
A Experimental source: phecohromocytoma
B R Ritamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
B Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A Title: Cloning and characterization of CDNA encoding a precursor for human adrenome
A; Reference number: JN0684; MUID:93343928; PMID:7688224
                                           C;Species: Homo_sapiens (man)
C;Daceate: 03-reb-1994 #text_change 20-Jun-2000
C;Daceasion: U2351; UN06464; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, Biochen. Blochen. Blochen. Brochen. Blochen. Blochen. Blochen. Blocken. Blochen. Blocker of Luman and M.;Itle: Genomic structure of human and M.;Itle: Genomic structure of human and M.;Reference number: JC2351; MUID:94354869; PMID:8074714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: pheochromocytoma
adrenomedullin precursor - human
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A; Residues: 1-185 <KIT>
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                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC2351
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A;Molecule type: DNA A;Residues: 1-643 <KAN>
A;Residues: 1-643 <KAN>
A;Residues: BMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10047.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Accession: T02702
A.Accession: T02702
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-776 CR0U>
A.Stesidues: 1-776 CR0U>
A.Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A.Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A.Experimental Source: cultivar Columbia
R.Inn, X.; Raul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D71870
hypothetical protein jhp0928 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: 12-Reb-1999 #sequence_revision 12-Feb-1999 #text_change 08-oct-1999
C;Accession: D71870
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g03240 [imported] - Arabidopsis thaliana
N.Alternate names: hypothetical protein T18E12.9
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C.Accession: T02702; A84446
R.Rounsley, S.D.; Lib, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, September 1998
A.Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Scatus: preliminary
A:Status: preliminary
A:Molecule type: DNA
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A;Cross-references: GB:AE002093; NID:g3548806; PIDN:AAC34478.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Note: T18E12.9
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                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 2; Length 643;
Pred. No. 0.61;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                               A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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                                                                                                                                                                                                                                                                                                                                                                                            67.18;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.1
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 GHEIYQYTDPD 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GHQIYQFTDKD 13
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Best Local Similarity
'...a 8; Conserve
                                                                                                                                                                                 A; Status: preliminary
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A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Keywords: amidated carboxyl end
C.Keywords: amidated carboxyl end
F.1-21/Domain: signal sequence #status predicted <PEU>
F.22-18/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAD>
F.22-41/Product: proadrenomedullin #status predicted <AMT>
F.94-143/Product: adrenomedullin #status predicted <AMT>
F.41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                           C, Accession: JN0766; PN0610
R; Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A; Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiy A; Reference number: JN0766; MUID:99384621; PMID:7690563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA ence
A; Reference number: S41600; MUID:94139945; PMID:8043068
A; Accession: S41600
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C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S41600
B;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
PEBS Lett. 338, 306-310, 1994
                                                                                                                                                                                                                                                C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Species: Synechocystis sp.
A. Variety: PCC 6803
C. Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C. Accession: S76069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 57; DB 2; Length 185; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 188;
0.014;
hes 0; Indels
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Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                                                                                                                          adrenomedullin precursor - rat
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Matches 10; Conservative
                                                     119 HQIYQFTDKD 128
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                  13
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                  HQIYQFTDKD
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A; Residues: 1-185 <SAK>
A; Accession: PN0610
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A; Residues: 1-188 <KIT>
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A; Accession: T04999
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Best Local Similarity
6; Conserve
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                  GB:AE001439; NID:94155505; PIDN:AAD06506.1; PID:9415550
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A;Experimental source: strain 168
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C;Superfamily: Bacillus subtilis hypothetical protein yycl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2
Pred. No. 40;
2; Mismatches
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                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 CARN>
A;Cross-references: GB:AE001522; GB:A;Experimental source: strain J99
C;Genetics: C;Genetics:
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Matches 8; Conserv
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hypothetical protein F19B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21106
R;Thomas, K.
Submitted to the EMBL Data Library, February 1996
A;Reference number: 219375
A;Reference number: 219375
A;Reference number: 210375
A;Reference: EMBL:269635; NID:91200023; PIDN:CAA93458.1; GSPDB:GN00022; CESP:F
A;Gross: CESP:19B6.3
A;Gene: CESP:19B6.3
A;Gene: CESP:19B6.3
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C;Date: 11.7un-1999 #sequence_revision 11.7un-1999 #text_change 01-Dec-2000
C;Accession: T09378; T04999
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, June 1999
A;Reference number: 216652
                                                                                                                                                                                                                                                                        A;Gene: CC2378
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolc
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R; Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.F.
submitted to the Protein Sequence Database, April 1998
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C;Genetics:
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A; Molecule type: DNA
A; Residues: 1-563 <BEV>
A; Cross-references: EMBL: AL078620; GSPDB:GN00062; ATSP:F23K16.250
                                                                                                                                                                                                                                                                                                                                                                           55.3%; Score 42; DB 2; Length 324; llarity 50.0%; Pred. No. 11; Conservative 2; Mismatches 4; Indels
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A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: A87249; MUID:21173698; PMID:11259647 A;Accession: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 444-563 <BE2>
A;Torss-references: EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F23K16.250 - Arabidopsis thaliana
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Pred. No.
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hypothetical protein [imported] - Staphylococcus aureus (strain N315)
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Matches 7; Conservative
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Best Local Similarity
'-has 8; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SA0139
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G83445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ygda [imported] - Lactococcus lactis subsp. lactis (strain IL1403) c; Species: Lactococcus lactis subsp. lactis c'Species: Lactococcus lactis subsp. lactis subsp. lactic lactic
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A; Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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A. Reference resistor: 121690
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1.467 < MLI>
A. Cross-references: EMBL: 281525; PIDN: CAB04258.1; GSPDB: GN00020; CESP: F33A8.4
A. Experimental source: Clone F33A8
A. Map Position: 2
A. Map Position: 2
A. Introns: 29/3: 159/2: 212/3: 243/3; 266/3; 365/3
C. Superfamily: Caenorhabditis elegans hypothetical protein F33A8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F33A8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T21690
R;Matthews, L.
                                                                                                                                                                                                                     Gaps
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                                                                                                                                              DB 2; Length 563;
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                                                                                                                                                                                                                     Indels
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                                                                                                                                       Score 42; DB 2
Pred. No. 21;
3; Mismatches
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Pred. No. 9.3;
0; Mismatches
                                                                                                                                          55.3%;
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                       2 GGHQIYQFTDKD 13
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GHQIYQFTDKD 13
A;Map position: 4
A;Introns: 118/3; 502/3
A;Note: T19P19:10
                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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368 YECHKLYQHSEK 379

RESULT 13 D89775

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Conserved hypothetical protein PA1607 [imported] - Pseudomonas aeruginosa (strain PAO C) Species: Pseudomonas aeruginosa (c) Species: Sastover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID: 20437337; PMID: 10984043
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-146 <STO>
A,Cross-references: GB:AE004588; GB:AE004091; NID:99947563; PIDN:AAG04996.1; GSPDB:GN
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"" Species: Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Accession: 109775
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
A;Hitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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C. Species: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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Pred. No. 28;
1; Mismatches
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Pred. No.
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C, Genetics:
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A, Residues: 1-260 <arn>
A, Cross-references: GB:AE001444; GB:AE001439; NID:g4154549; PIDN:AAD05628.1; PID:g415455
B, Experimental source: strain J99
C, Genetics:
A; Gene: jhp0046
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Query Match
52.6%; Score 40; DB 2; Length 260;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels

0; Gaps

0;

1 YGGHQIYQFTD 11 :|||| || || 194 FGGHQNAQFND 204

qq οy

Search completed: October 14, 2003, 08:40:48 Job time: 10.3864 secs

us-09-931-700-2.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 14, 2003, 08:35:36; Search time 4.13636 Seconds (without alignments) 147.798 Million cell updates/sec Run on:

US-09-931-700-2 76 1 YGGHQIYQFTDKD 13 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	pti	P35318 homo sapien	rattu		pos	cant				P27028 flavobacter	P51862 saccharomyc	P58502 pyrococcus							053656 mycobacteri							085467 bacillus ĉe					33		0		
SUMMARIES	ID	ADML_HUMAN	ADML_RAT	ADML_PIG	ADML_BOVIN	ADML_CANFA	ADML_MOUSE	SYN_DROME	SYH_METTH	PPCE_FLAME	ROM2_YEAST	TKSU_PYRKO	CDPK_DAUCA	DEXT_STRDO	AMY_STRVL	HIS6_VIBCH	SI7D_HUMAN	SI7D_MOUSE	Y205_MYCTU	CBPT_THEVU	SAHH_CAUCR	DNAA_TREPA	SNXI_HUMAN		YNL5_YEAST	GRIA_BACCE	Y379_HUMAN	TRI_THEAC	AMY_STRGR	AMY_STRLM	VATF_DESSY		YFJY_ECOLI	UL31_HSV11	
	DB	Н	М	Н	Н	Н	Н	-1	-	Н,	Н.	Н	-	—		Н	_		Н		Н	~	Н	, -1	-1	-	Н.	—	-	Н	H	Н	H	-	
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dР	Query Match	75.0	75.0	LO.	æ	68.4	67.1	59.6	51.3	51.3	51.3	50.0	50.0	50.0	49.3	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.7	8	48.0	48.0	47.4	47.4	47.4	47.4	
	Score	57	57	57	52	25		45.5	37 C	5 0 (т с т	æ F	86		37.5	37	37	37	37	37	37	37	37	37	3.7	37	7 2 2		36.5	_	36	36	36	36	
	Result No.	н	(4	m	♥ 1	ഗ	ופ	7	x	,	7 7	7.	77	L1	14	15	16	17	89 ¢	61	20	21	77	57	4, r	77	9 1	17	870	67	30	31	32	33	

Q8cze6 oceanobacil P46831 mycobacteri Q82292 s glucosami Q93831 candida alb Q27421 drosophila P4795 mycoplasma Q40519 nicotiana t Q40070 hordeum vul P10690 spinacia ol P25210 petromycon P35594 bacillus su Q97vp5 sulfolobus
MUEL_OCEIH ACEA_MYCLE GLMZ_SALTI EARP_CANAL OSP_DROME Y149_MYCGE PSBR_HORVU PSBR_RORVU PSBR_RSFOL CBFA_PETIOL THIE_BACSU SFSA_SULSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR AGENTS. NUMERCUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSICLOGIC CONTROL OF FIGUD AND ELECTROLITE HOMEOSTASIS. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP PITHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN FITHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN ACTH COMPLEMENT THEIR TYPOTENSIVE EFFECTS IN BLOOD.
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20053666; PubMed=10588445; Champion H.C., Nussdorfer G.G., Kadowitz P.J.; "Structure-activity relationships of adrenomedullin in the circulation and adrenal gland."; Regul. Pept. 85:1-8(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (G-42 PROVIDE AMIDE GROUP).
                                                                               Matsuo H., Eto T.; "Adrenomedullin: a novel hypotensive peptide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone; Amidation; Cleavage on pair of basic residues; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTC
ADRENAL MEDULIA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                        Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREPROAM C-TERMINAL FRAGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO: GO: 0005615; C: extracellular space; TAS.
GO: GO: 0005615; C: extracellular space; TAS.
GO: GO: 0005625; C: soluble fraction; TAS.
GO: GO: 0005717; P: CAMP biosynthesis; TAS.
GO: GO: 0007156; P: circulation; TAS.
GO: GO: 0007565; P: pregnancy; TAS.
GO: GO: 0005611; P: response to wounding; TAS.
GO: GO: 0005611; P: response to wounding; TAS.
GO: GO: 0007165; P: signal transduction; TAS.
InterPro: IPR001710; Adrenomedullin.
Pfam. PF02039; Adrenomedullin; 1.
                                                                                                                                                        Biochem. Biophys. Res. Commun. 192:553-560(1993).
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                                                                                                                                                                                                                                                                                          "Proadrenomedullin-derived peptides.";
Front. Neuroendocrinol. 19:100-127(1998).
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AMIDATION
TISSUE=Pheochromocytoma;
MEDLINE=93249425; PubMed=8387282;
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BC015961; AAH15961.1; --
D43639; BAA07756.1; ALT_SEQ.
                                                                                                                                                                                                                                          MEDLINE=98240137; PubMed=9578982;
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Genew; HGNC:259; ADM.
                                                                                                                                    pheochromocytoma.";
                                                                                                                                                                                                                                                                         Samson W.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N., Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.; Discovery of adrenomedullin in rat ischemic cortex and evidence for its role in exacerbaing focal brain ischemic damage."; Proc. Natl. Acad. Sci. Us.A. 92:11480-11484(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuo H., Eto T.; "Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                     Gaps
                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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                                                                                                  ;0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY
                                                           75.0%; Score 57; DB 1; Length 185; 100.0%; Pred. No. 0.0068; Pred. No. 0.1068; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADRENOMEDULLIN,
PREPROAM C-TERMINAL FRAGMENT
                                20420 MW; 64C7D2A0B4654DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, I
HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
   -> R (in dbSNP:5005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypotensive peptide.";
Blochem. Blophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; TISSUE-Adrenal gland; MEDLINE=93384621; PubMed-7690563;
                                                                                                                                                                                                                                             185 AA
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                FTIG=VAR
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InterPro; IPR001710; Adrenomedullin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=96102137; PubMed=8524787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
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EMBL; U15419; AAB60519.1; -.
                                                                            Local Similarity 100.
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                        122 HQIYQFTDKD 131
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91
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185
                              185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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45
94
149
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P43145;
                              SEQUENCE
                                                              Query Match
VARIANT
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                                                                                           Matches
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SIMILARITY).

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-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
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                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                    (BY SIMILARIEL).
AMIDATION (G-144 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
              AMIDATION (G-42 PROVIDE AMIDE GROUP) (BY SIMILARITY).
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Hormone; Amidation; Cleavage on pair of basic residues; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; "Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)"; FEBS Lett. 351:35-37(1994)
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PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                              Score 57; DB 1; Length 185;
Pred. No. 0.0068;
Mismatches 0; Indels
                                                                                35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                     188 AA.
                                                                                                                                                 0; Mismatches
SIMILARITY
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Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                  75.0%; Score
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TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                  (BY
                                                                                185 AA; 20636 MW;
                                                                                                                                 100.08;
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                                                                                                                                                 10; Conservative
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                                                                                                                                 Best Local Similarity
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               41
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               MOD_RES
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the Buropean Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARIII.
PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98244567; PubMed=9585168;
Barker S., Wood E., Clark A.J.L., Corder R.;
"cloning of bovine preproadrenomedullin and inhibition of its basal expression in vascular endothelial cells by staurosporine.";
Life Sci. 62:1407-1415(1998).
-i- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
         BY SIMILARÍTY.

AMIDATION (G-42 PROVIDE AMIDE GROUP).

AMIDATION (G-147 PROVIDE AMIDE GROUP).

71749460F55660A61 CRC64;
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(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                            Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HORTMONE; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 1; Length 188; Pred. No. 0.052;
                                                                                      Length 188;
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIRCULATION COATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                    Score 57; DB 1; 1
Pred. No. 0.0069;
                                                                                                                                                                                                                                                          188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDUIN.
                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ001613; CAA04866.1; -
                                                         20893 MW;
                                                                                    75.0%; ; 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20981 MW;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                    Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                               122 HQIYQFIDKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
146
188
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                                       146
                                                                                                                                                4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
           110 1
41
146 1
188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Aorta;
                                                                                                                                                                                                                                                      ADML_BOVIN
062827;
                           MOD_RES
MOD_RES
SEQUENCE
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            DISULFID
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KO M.S.H.;
                         ADML_MOUSE
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PROPEP
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     RESULT 6
                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                          ono Y., Kojima M., Okada K., Kangawa K., "cDNA cloning of canine adrenomedullin and its gene expression in the heart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
-1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 BY SIMILARITY.
PEPTIDE 22 41 PROADRENOMEDULLIN N-20 IERMINAL PEPTIDE.
                                                                                                      16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-42 PROVIDE AMIDE GROUP) (BY SIMILARITY).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                            Imoto I., Jougasaki M.; "Cloning of cDNA encoding canine adrenomedullin."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 1;
Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U96127; AAD09957.1; -.
INTERPO, INTEROUTO, Adrenomedullin.
Pram; PF02039; Adrenomedullin, 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                   MEDLINE=99002704; PubMed=9788655;
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0
                                                                    ADML_CANFA STANDAKU;
077559; Q9TVC9;
16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF045773; AAD05423.1; -.
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                      122 HQIYHFTDKD 131
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 4 HQIYQFIDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HQIYQFTDKD 13
                                                                                                                                                             Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=9615;
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PROPEP
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                                                              ADML_CANFA
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                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression of adrenomedullin, a hypotensive peptide, in the trophoblast giant cells at the embryo implantation site in mouse."; Dev. Biol. 203:664-275(1988).
-1- FUNCŢION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HORMONE, Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL
1
21
BY SIMILARITY.
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O
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Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 1; Length 184;
Pred. No. 0.076;
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C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
     184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADRENOMEDULLIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97092892; PubMed-8938454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D78349; BAA11367.1; -. EMBL; U77630; AAB36535.1; -.
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90.08;
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Best Local Similarity 90.v.,
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 HOLYOLTDKD 129
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                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS SYN-S AND SYN1-RT).
STRAIN=Berlin, TISSUB=Head;
MEDLINE=96209149; PubMed=8627354;
Klagges B.R.E., Heimbeck G., Godenschwege T.A., Hofbauer A.,
Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Invertebrate synapsins: a single gene codes for several isoforms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOId=024546-2; Sequence=VSP_006324;
-1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM.
-1- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform Syn-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980 AA; 102799 MW; E6037A2A4804F944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.9%; Score 45.5; DB 1; 52.6%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms=2;
                                                                                               024546; Q24545;
30-MAY-2000 (Rel. 39, Created)
20-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flyase; FBG00004575; Syn.
InterPro; IPR001359; Synapsin.
Pfam: PF02078; Synapsin. 1.
PRINTS: PR01368; SYNAPSIN.
PROSITE; PS00415; SYNAPSIN.
PROSITE; PS00416; SYNAPSIN. 1; FALSE_NEG.
Synapse; Neurone; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId-Q24546-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila.";
... Neurosci. 16:3154-3165(1996).
-!- SUBCELLULAR LOCATION: SYNAPSE.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 YGGVPSINSLHSIYQFQDK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X95453; CAA64723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X95453; CAA64722.1; -.
HSSP; P17599; 1AUX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.00,
Conservative
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-Syn1-RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Syn-S;
                                                                                                                                                                                                                                                                  SYN OR SYN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchner E.;
                                                                       SYN_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                       Synapsin.
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RESULT 7
SYN_DROME
                                                                       S THE THE TENT TO BE THE TENT TO THE TENT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A MEDLINE-98037514; PubMed-9371463;
A MEDLINE-98037514; PubMed-9371463;
A Aldrager F., Bashlaradeh R., Blakely D., Cook R., Gilbert K.,
A Aldrager F., Bashlaradeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shime G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
C. -I CATALYTIC ACTIVITY: ATP + L.histidine + tRNA(His) - AMP +
diphosphate + L.histidyl-tRNA(His).
C. -I SUBCELJULAR LOCATION: Cytoplasmic.
C. -I SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Prolyl endopeptidase precursor (EC 3.4.21.26) (Proline-specific endopeptidase) (PSE) (Post-proline cleaving enzyme) (PE).
                                                         15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                         Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.3%; Score 39; DB 1; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 AA; 48019 MW; 8388A5975A017535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 AA.
425 AA
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                                                                                                                                                                                                                                                                                                                             Methanobacteriaceae; Methanothermobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HANDE, ME_00127; -; 1.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004154; Hiss.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR006195; tRNA_ligase_II.
Pfam; PF03129; HGTP_anticodon; 1.
Pfam; PF00587; tRNA-synt_2b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000811; AAB84750.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0442; hiss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 HQIYQFTDK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 NQIYHFTDK 68
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Delta H;
                                                                                                                                                                                                                           HISS OR MTH244.
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P27028;
   SYH_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                         (HisRS
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PRT; 1356 AA

STANDARD;

9

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ROM2_XEAST
P51862;
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92176159; PubMed=1840588;
Yoshimoto T., Kanatani A., Shimoda T., Inaoka T., Kokubo T., Tsuru D.;
"Prolyl endopeptidase from Flavobacterium meningosepticum: cloning and sequencing of the enzyme gene.";
J. Biochem. 110:873-878(1991).
                                                                                                                                                                                      Flavobacterium meningosepticum (Chryseobacterium meningosepticum).
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Hydrolysis of Pro-|-Xaa >> Ala-|-Xaa in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC0EDCBABB328256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROLYL ENDOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00126; Peptidase_S9: 1.
Pfam: PF02897; Peptidase_S9: 1.
PRINTS; PR00862; PR0LIGOPTASE.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
Hydrolase; Serine profease; Periplasmic; Signal.
                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> C (IN REF. 2).
R -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 39;
1; Mismatches
                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001375; Peptidase_89.
InterPro; IPR004106; Peptidase_89_N.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR00379; Ser_estrs_site.
                                        Flavobacteriaceae; Chryseobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78707 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D10980; BAA01755.1; -. EMBL; X63674; CAA45213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           587
                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; JX0194; JX0194.
HSSP; P23687; 1QFM.
MEROPS; S09.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556
675
110
587
705 AA;
                                                                                                                                                                                                                                                                                                                                                          oligopeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD; S0004363; ROMZ.

GO; GO:0005934; C:bud tip; IDA.

GO; GO:0005894; E:stonal tip; IDA.

GO; GO:0004871; E:stonal transducer activity; IDI.

GO; GO:0007117; P:bud growth; IPI.

GO; GO:0007047; P:cell wall organization and biogenesis; IPI.

GO; GO:0000283; P:establishment of cell polarity (sensu Sacch. . ; IP)

GO; GO:0000284; P:small GTPase mediated signal transduction; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96208506; PubMed=8641285;
Ozaki K., Tanaka K., Imamura H., Hihara T., Kameyama T.,
Nonaka H., Hirano H., Matsuura Y., Takai Y.;
"Romlp and Rom2p are GDP/GIP exchange proteins (GEPs) for the Rholp small GPP binding protein in Saccharomyces cerevisiae.";
EMBO J. 15:2196-2207(1996).
-I- FUNCTION: STIMULATES THE EXCHANGE OF RHO1 GDP-BOUND FORM INTO
                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00741; DH_1; FALSE_NEG. PROSITE; PS50010; DH_2; 1. Guanine-nucleotide releasing factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001180; Citron.
InterPro; IPR00180; Citron.
InterPro; IPR00131; GDS_CDC24.
InterPro; IPR00131; RhoGEF.
Pfam; PF00780; CNH; 1.
Pfam; PF00610; DEP; 1.
SMART; SM00036; CNH; 1.
SMART; SM00049; DEP; 1.
                                                                  RHO1 GDP-GTP exchange protein 2. ROM2 OR YLR371W OR L8039.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U19103; AAB67564.1; -. PIR; S51389; S51389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00325; RhoGEF; 1
                                                                                                                                                                                                                                                                                                                                                                                         Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP-BOUND FORM
                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                           NCBI_TaxID-4932;
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POLY-ASN.

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ROM2_YEAST RESULT 10

50 GGHIVYOF 57

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STANDARD;
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PIR; T14335; T14335.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
                                                                                                                CDPK_DAUCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                          CDPK_DAUCA
                                                                                                                                                                                                                                                                                                                                                                                                                         Choi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kannan Y., Koga Y., Inoue Y., Haruki M., Takagi M., Imanaka T., Morikawa M., Kanaya S.;
Morikawa M., Kanaya S.;
"Active subtilisin-like protease from a hyperthermophilic archaeon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBGNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- MISCELLANEOUS: Thermostable; high activity at 80 degrees Celsius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TK-SUBTILISIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a form with a putative prosequence.",
Appl. Environ. Microbiol. 67:2445-2452(2001).
-!- FUNCTION: Has a borad substrate specificity with a slight
preference to large hydrophobic amino acid residues at the Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Calcium-binding; Zymogen; Signal.
                                                                                     Score 39; DB 1; Length 1356;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 38; DB 1; Length 422; 75.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
329 336 POLY-HIS.
632 635 POLY-ASP.
1356 Aa; 152595 MW; 5FBC542114E7BC92 CRC64;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           843255BCD806DB71 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimal pH is 9.5.
SIMILARITY: Belongs to peptidase family S8
                                                                                                                                                                                                                                                                                                                                                TKSU_PYRKO STANDARD; PRT; 422 AA. P58502; 0977F5; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last_annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tk-subtilisin precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21268834; PubMed=11375149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43785 MW;
                                                                                          51.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB056701; BAB60701.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus kodakaraensis.
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           position.
COFACTOR: Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
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496 HEVYEFTD 503
                                                                                                                                                                                      4 HQIYQFTD 11
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=69014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                               TKSU_PYRKO
                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                         calcium-dependent protein kinase: homology to calcium/dalmodulin-dependent protein kinases and to calmodulin-dependent protein kinases and to calmodulin."; plant Mol. Biol. 17:581-590(1991).

INTO TON: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT INVOIVE CALCIUM AS A SECOND MESENGER.

--- ENZYME REGULARION: ACTIVATED BY CALCIUM, AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

--- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                          Daucus carota (Carrot).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; campanulids; Apiales; Apiaceae; Daucus.

NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 108-532 FROM N.A. MEDINE-9203674; Pubmed-1912486; Suen K.-L., Choi J. H.; "Isolation and sequence analysis of a cDNA clone for a carrot "Isolation and sequence analysis of a cDNA clone for a carrot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAMK SUBFAMILY.
SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F03E6F036A0AE348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
EF-HAND 4 (POTENTIAL).
                                       01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY). ATP (BY SIMILARITY).
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 532 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00018; EF HAND; 4.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q63450; 1A06.
InterPro; IPR0002048; EF-hand.
InterPro; IPR0002049; PF-hand.
InterPro; IPR000290; Ser_thr_pkinase.
Pfam; PF00036; efhand; 4.
Pfam; PF00069; pkinase; 1.
ProDom; PD000012; EF-hand; 2.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00054; EFh; 4.
SMART; SM00220; S_TKC; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60065 MW;
                                     24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X56599; CAA39936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465
500
532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                    ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-9422401; PubMed-8021165; Wanda S.-Y., Curtiss R. III; PubMed-anacterization of Streptococcus sobrinus dextranase produced in recombinant Escherichia coli and sequence analysis of the dextranase gene."; J. Bacteriol. 176:1839-1850(1994).

-!-FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE PELLICLE-COATED TOOTH SURFACE.

-!-CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic linkages in dextran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
-!- MISCELLANEOUS: The activity of this enzyme is optimal at pH 5.3 and at 39 degrees Celsius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1308 1308 AMIDE-LINKED TO CELL WALL (POTENTIAL)
1337 AA; 143298 MW; B494275A77A2E3D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;
Signal; Plasmid.
                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPXTG SORTING SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEXTRANASE. REMOVED BY SORTASE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 1337; Pred. No. 1.1e+02;
50.0%; Score 38; DB 1; Length 532; 60.0%; Pred. No. 44;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
                                    2;
                                                                                                                                                                                                                                                                                                                                                 Streptococcus downei (Streptococcus sobrinus)
                                                                                                                                                                                                    PRT; 1337 AA.
                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
STRAIN=6715 / UAB66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PÍAM; PF00746; Gram_pos_anchor; 1.
TIGRFAMS; TIGR01167; LPXIG_anchor; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR006192; LPXTG.
                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M96978; AAA21772.1; -.
                                  6; Conservative
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1308
1337
1309
1308
                                                                                              458 HQAFQYFDKD 467
                                                                       4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, 15-SEP-2003 (Rel. 42,
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                .ucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                     Plasmid pYA902.
                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=6715
                                                                                                                                                                                                 DEXT_STRDO P39653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                    Matches
                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                        Virolle M.-J., Long C.M., Chang S., Bibb M.J.; "Cloning, characterisation and regulation of an alpha-amylase gene
                                                                                                                                                                                                                                                                                                                                                          linkages in oligosaccharides and polysaccharides.
-!- INDUCTION: BY MALTOSE, AND REPRESSION BY GLOCOSE.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    э;
                                                                                                                                                                                                                                                                                                      from Streptomyces venezuelae.";
Gene 74:321-334(1988).
-!- CATALYIIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 569;
                                                                                                                                  Streptomyces violaceus (Streptomyces venezuelae),
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                 01-AUG-1991 (Rel. 19, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWART; SM00632; Aamy_C; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F SIMILARITY.
F SIMILARITY.
F SIMILARITY.
F SIMILARITY.
I4CA5B1D56720043 CRC64;
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569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-AMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JS0101, JS0101.
HSSP: P29957; JAOM.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006648; Alpha_amyl_C:
InterPro; IPR006647; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR005044; CBD_4.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha_amylase; 1.
Pfam; PF001806; alpha_amylase_C; 1.
Pfam; PF00686; CBM_20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.3%; Score 37.5; 50.0%; Pred. No. 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 15068;
MEDLINE=89232724; Pubmed=3266752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0110; ALPHAANTLASE.
PRODOM: PD001568; CBD-4; 1.
SMART; SMO0642; Aamy; 1.
SMART; SMO0632; Aamy.C; 1.
                                 01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 YGSPDVHSGYEWTDKD 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M25263; AAB36561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YGG---HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
                                                 01-AUG-1991 (Rel. 19, 01-APR-1993 (Rel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 8; Conserv
                                                                                                   glucanohydrolase).
                                                                                                                                                                                      NCBI_TaxID-1936;
 AMY_STRVL
P22998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
SEQUENCE
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Gaps

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3; Indels

4; Mismatches

41.78;

Conservative

Best Local Similarity Matches 5; Conserv

2 GGHOIYOFTDKD 13

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RESULT 15

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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAINFEI TOR Ni6961 / Serotype 01;
STRAINFEI TOR Ni6961 / Serotype 01;
MEDLINE=2040683; PubMed=10952301;
Heidelberg J.F., Eisen D.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Vamathevan J., Bass S., Oin H., Dragoll I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).

"Induce 406:477-483(2000).

"Induce 406:477-483(2000).

"Induce 406:477-483(2000).

"Induce 105, AICAR and glutamate. The hist subunit catalyzes the Cyclization activity that produces IGP and AICAR from PRFAR using the ammonia provided by the hisH subunit (By similarity).

"Induce ACTIVITY: 5-{(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine - imidazole-glycerol phosphate + 5-aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)0.

"PATHWARY: Haltidine blosynthesis, fifth step.

"SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

"SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (IMSP synthase Subunit hisF) (IMSP subunit hisF) (IMSP subunit hisF) (IMSP subunit hisF) (IMSP synthase Subunit hisF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .:
0
                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 AA; 28338 MW; F722BBC43BEB153C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histidine blosynthesis; Lyase; Complete proteome.
               257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.7%; Score 37;
66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR003009; FWN_enzyme.
InterPro: IPR006062; His_biosynth.
InterPro: IPR004651; HisF.
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00977; His_biosynth; 1.
TIGREAMS; TIGR00735; hisF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004193; AAF94297.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; E82238; E82238.
TIGR; VC1138; -.
HAMAP; MF_01013; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                            Vibrio cholerae.
                                                                                                                                                                                                                                                                        NCBI_TaxID=666;
                 HIS6_VIBCH
Q9KSW8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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HIS6_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Job time : 7.13636 secs

Search completed: October 14, 2003, 08:39:09

GOYOVYOFT 146

138

2 GGHQIYQFT 10

QY Db

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095KPO;
01-DEC-2001 (TrEMBLrel. 19, Created)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADRENOMEDULLIN.
Sus scrofa (Pig).
                                                                                  SEQUENCE
                                                                                                                                                                                                                                          39.
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                                                                                                                                                                                                                                                                                                                            Q9TRZ6
                                                                                                                                                                                                                                                                                                          RESULT 1
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                                                                                                                                                                                                                                                                                                                                     δ
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Q8inm4 drosophila
Q24544 drosophila
Q29vh15 drosophila
Q8inm6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9x5r9 streptomyce
Q9zkk7 helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9ewq4 streptomyce
Q45612 bacillus su
Q9a5r9 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        081050 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8rcv8 thermoanaer
Q19582 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8mxj0 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9trz6 sus scrofa
Q95kp0 bos taurus
                                                    October 14, 2003, 08:36:06; Search time 17.4318 Seconds (without alignments) 192.446 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                           830525
         Compugen Ltd.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                        830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95KP0
Q55549
Q81NM4
Q24544
Q9VH15
Q81NM6
Q81NM6
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Q45612
Q9A5R9
Q8RCV8
Q19582
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Q8MXJ0
                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TRZ6
                                                                                                                                                                                                                                                                 sp_archa:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                         sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                  sp_vertebrate:*
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sp_phage:*
                                                                                                           1 YGGHQIYQFIDKD 13
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
sp_rodent:*
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16
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                                                                                                                                                                                                                                                                                                                                                                                                    sp_rvirus:*
                                                                                                                                                                                                                                                                                                                   sp_mamma]:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                       sp_virus:*
                                                                                        US-09-931-700-2
76
                                                                                                                                                                                                                                                          SPTREMBL_23:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2231
173
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280
324
326
350
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45.5
45.5
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                                   OM protein
                                                                                                                                                        Searched:
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                                                     Run on:
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09zn14 helicobacte
08vtb6 helicobacte
08vtb3 helicobacte
08vtb3 helicobacte
08vte5 helicobacte
08vte8 helicobacte
08cte8 helicobacte
01652 caenorhabdi
                    09chs8 lactococcus
062214 caenorhabdi
099x71 staphylococ
08nyq7 staphylococ
076322 loligo peal
                                                                                                                                               Q8kc18 chlorobium
Q9bsu7 homo sapien
Q991f0 mus musculu
                                                                                                                                                                      Q8s011 oryza sativ
Q943e0 oryza sativ
Q8chg6 mus musculu
                                                                 Q9ugx0 homo sapien
Q9i3b4 pseudomonas
                                                                                                                                                                                           015031 homo sapien
Q9usq7 schizosacch
Q8epg1 oceanobacil
 Q9sv96 arabidopsis
        O9utt2 schizosacch
O91474 lactococcus
                                                                               Q8vte0 helicobacte
                                                                                                   0897E3
0897L3
0897E5
0807E8
016622
0965L2
08KCL8
              Q9L474
Q9CHS8
O62214
                                                                                                                                                                      Q8S011
Q943E0
Q8CHG6
                                                                                      Q9ZN14
Q8VTB6
                                                                       Q913B4
Q8VTE0
                                   Q99X71
Q8NYQ7
O76322
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                                                        076323
Q9UGX0
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44444422
444444444
40.54
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ALIGNMENTS

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MEDLINE-96157714; PubMed=8576091; MEDLINE-96157714; PubMed=8576091; MEDLINE-96157714; PubMed=8576091; Lohiki Y., Klamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.; Distribution and characterization of immunoreactive adrenomedullin porcine tissue, and isolation of adrenomedullin [26-52] and adrenomedullin [34-52] from porcine duodenum."; J. Biochem. 118.765-770(1955). InterPro; IPRO01710; Adrenomedullin. Pro2039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                  Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 0.0097;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 AA; 3063 MW; B8DC7FA18D8B3D90 CRC64;
                    27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00801; ADRENOMEDULN
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Query Match
Best Local Similarity
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                                                                                                                                                                                         QBINM4
                                 Matches
                                                                                                                                                       RESULT
Q8INM4
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                                                                                                                                                                SEQUENCE FROM N.A.
Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
Kangawa K., Eto T.;
"ADRENOMEDULLIN (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96127529; PubMed-8590279; Raneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; Sequence analysis of the genome of the unicellular cyanobacterium Sequence analysis postinon PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 6; Length 188; Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055107; BAB62176.1; -
Interpret: IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:109-136(1996).

BMBL, D63999; BAA10047.1; --
Hypothetical protein; Complete proteome,
SEQUENCE 643 AA; 68369 MW; 1EE9001D332B411 CRC64;
                                                                                                                                                                                                                                                                                                                                          20963 MW; 6102E69A756DCA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein slr0168.
 (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                                                                                        FROM BOVINE ADRENAL MEDULLA."
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90.0%;
 01-DEC-2001 (TremBLrel. 19,
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||| |||||
|122 HQIYHFIDKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HQIYQFTDKD 13
                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                          188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1148;
                                                                                                                                    NCBI_TaxID=9913;
                                 Adrenomedullin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                          SECUENCE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Fvans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Fvans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfelfifer B.D.,
RA Bardon R.C., Rogers Y.H., Blazel R.G., Change M., Pfelfifer B.D.,
RA Beson K.Y., Basu A.A. M. H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y., Basu A.A. Baxendale J., Bayraktaroquel L., Beasley E.M.,
RA Beson K.Y., Basu A.A., Baxendale J., Bayraktaroquel L., Beasley E.M.,
RA Beson K.Y., Betchan M.R., Bounk J., Brottier P.,
RA Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chadra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Perriar S., Pletz S.,
RA Godon K., Doug L.E., Downess M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Godor K., Gong F. Gorrell J.H., Wel M. H., Ibeywam C.,
RA Hostin D., Houston K.A., Helman T.J., Hermandez J.R., Harris M.,
Alasko P., Lei Y., Levitsky A.A., Li J., Marris M.,
RA Hostin D., Houston K.A., Nahan T.J., Hermandez J.R., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Musher D.M., Nelson D.L.,
RA Bazzolo M., Pittman G.S., Pan S., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I. Simpson M., Strong R., Sun E.,
Sylener E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Sylener E., Spradling A.C., Stapleton M., Strong S., Yao Q.A., Ye J.,
RA Shen S., Woodager, Worley K.C., Wu D., Yang S., Zao Q.A., Ye J.,
Ra Jener K., Wassarman D.A., Weinstock G.W., Weissenbach J.,
Walls M. Weissenbach J. S., Zhong W., Zhong Y., Zhong Y., Weilliams S.W., Woodager, Worley W., Zhong Y., Zhun G., Sheng C., Stence SH, Shine S., Shong S., Shon M., Sheng X.H., Zhong F.N., Zhong 
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                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Score 51; DB 16; Length 643; Pred. No. 3;
                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG3985-PC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       348 AA.
                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                          8; Conservative
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                                                                                                                                                                                                                                    447 GHEIYOYIDPD 457
                                                                                                                                                     3 GHQIYQFTDKD 13
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Query Match
Best Local 9
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                                            Matches
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MEDLINE=96209149; PubMed-8627354;
Klagges B.R., Heimbeck G., Godenschwege T.A., Hofbauer A.,
Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
                                                                                                                                                                                    Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kroumiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M., J., Smith B., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Invertebrate synapsins: a single gene codes for several isoforms in
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., Marthcosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfelifer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota: Metazoa: Arthropoda: Hexapoda: Insecta; Pterygota; Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003686; AAN13464.1; -
SEQUENCE 348 AA; 38321 MW; 8FA837EF9A438134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HOMOLOGUS to synapsin II (Fragment).
SYN OR SYN2 OR CG3985.
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DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.9%; Score 45.5; I 52.6%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila.";
J. Neurosci. 16:3154-3165(1996).
EMBL; X95454; CAA64724.1; -.
HSSP; P17599; 1AUX.
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Pfam; PF02078; Synapsin; 1.
Pfam; PF02750; Synapsin_C; 1.
PRINTS; PR01368; SYNAPSIN_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.67
Watches 10; Conservative
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Batdon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,
R.A. Bardon R.C., Baxter E.G., Helt G., Nalson C.R., Gabor G.L.
R.A. Ballow R.M., Baru A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
R. Besson K.Y., Bennes P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Borkova D., Botchan M.R., Bouch J., Bhandari D., Bolshakov S.,
R. Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Burtis R.C., Busam D.A., Lewins M., Davies P., Brotcher A., Chandra I.,
R.A. Bodson K., Doup L.E., Downes M., Diqan-Rocha S., Dunkov B.C., Dunn P.
R.A. Bodson K., Doup L.E., Downes M., Diqan-Rocha S., Dunkov B.C., Dunn P.
R.A. Bodson K., Doup L.E., Downes M., Diqan-Rocha S., Dunkov B.C.,
R.A. Gooff F. Gorrell J.H., Galz, Galbart W.M., Glasser K.,
Allock A., Gooff F. Gorrell J.H., Wei W.H., Ibeywam C.,
R.A. Hostin D., Harvey D., Hediman T.J., Hernandez T.R., Hernandez T.R., Hernandez T.R.,
R. Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C.,
Allali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Allakov P., Lei Y., Levitsky A.A., Li J., Mirony D.M., Nelson D.L.,
Ment S.M., Moy M., Murphy B., Murphy L., Mirony D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nosskern D.R., Purl V., Realson D.L.,
R. Rainert R., Remington K., Sauders R., San H.,
Spier E., Sdentria G.S., Pan S., Pollard J., Purl V., Reese M.G.,
R. Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
R. Shien E., Saradling A.C., Simpson M., Strong R., Shu B.C.,
R. Hillams S.M., Woodseff, Worlk W., Yang S., Yao Q.A., Ye J.,
R. Janeng R.H., Wessamman D.A., Weinschoff, S., Bang S., Bang S., Bang S., Bang S., Woods
                                                                                 1;
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodsson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
       DB 5; Length 388;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                             5.
                                                                                                                                                                                                                                                                                                                                                                                                                 443 AA.
Score 45.5; D
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=20196006; PubMed=10731132;
                                                                                                                                              1 YGG-----HQIYQFTDK 12
                                                                                                                                                                                                                    81 YGGVPSINSLHSIYQFQDK 99
   59.98;
52.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13,
                                                                         10; Conservative
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003
CG3985-PD.
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RESULT 8
O81050
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SEQUENCE FROM N.A.

WE SEQUENCE FROM N.A.

WE SEQUENCE FROM N.A.

WE SEQUENCE FROM N.A.

WE SEQUENCE FROM N.B.

WE SEQUENCE R.B.

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                                                                                                                                                                                                    Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.W.J., Smith B., Shu S., Smutniak F., Whitfield E., Ansburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pardgas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith B.O., Ventler J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45.5; DB 5; Length 443; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003686; ARF54506.2; -.
Flymase; PRO00046575, Syn.
SEQUENCE 443 AA: 47645 MW; DIB10DA3E655C59D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG3985-PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 YGGVPSINSLHSIYQFQDK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YGG-----HQIYQFTDK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 52.64
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                   SEQUENCE FROM N.A.
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A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Houstin D., Houston K.A., Howland T.J., Well M.H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Lei Y., Lei Y., Li J., Li J., Lilang Y., Lin X.,
And Liu X., Mattei B., McIntosh T.C., McLodd M.P., McPherson D.,
McMut S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Ra Reinert K., Sten Kiamos I., Simpson M., Skrupski M.F., Smith T.,
Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Rh Sheng X.H., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Rh Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rh Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celliker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Banso J., An H., Baldwin D., Banson J., Beeson K.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenort L.B., Dietz S.M.,

Bodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Reriera S., Frise E., Galle R.P., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Lbegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Rolltosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouancavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of prosophila melanogaster genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.9%; Score 45.5; DB 5; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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537 AA; 57691 MW; 782BE20B4BE60220 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 21;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YGG-----HQIYQFIDK 12
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nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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776 AA.

PRT;

PRELIMINARY;

081050

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Gaps

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Indels

5;

Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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8; Conservative
                                                                                                                                                                                              PRELIMINARY;
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                                                                               GGHGIYQFYD 75
                                        2 GGHQIYQFTD 11
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                                                                                   99
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                                                                                                                                                                                                                     Q92KK7;
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Matches
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=cv. Columbia;

STRAIN=20083487; PubMed=10617197;

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana ";
                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyladons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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STRAIN-NRRL 2564;
MEDINE-9201491; Pubmed=10099135;
MAO Y., Varoglu M., Sherman D.H.;
"Molecular characterization and analysis of the biosynthetic gene cluster for the antitumor antibiotic mitomycin C from Streptomyces lavendulae NRRL 2564.";
Chem. Biol. 6:251-263(1999).
EMBL; AF127374; AAD32724.1; -.
SEQUENCE 514 AA; 55697 WW; 888C7E685B8B2F2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.2%; Score 45; DB 10; Length 776; 66.7%; Pred. No. 38;
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Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AC003313, AAC3478.1; -1 InterPro; IPR004342; EXS_Cterm. InterPro; IPR004331; SPX. Pfam; PF03124; EXS. 1. Pfam; PF03124; EXS. 1. SEQUENCE 776 AA: 89775 MW; BE30603ACFADD14E CRC64;
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Last annotation update)
                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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80.0%;
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STRAIN=cv. Columbia;
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Best Local Similarity
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                                                                                   At2g03240 protein.
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                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                          AT2G03240
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MEDLINE=99120557; PubMed=9923682;
MEDLINE=99120557; PubMed=9923682;
MAID R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                             Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
Trust T.J.;
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Pred. No. 1.7e+02;
2; Mismatches 4; Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein C0869.1.
                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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PRT; 2231 AA.
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Nature 397:176-180(1999).
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InterPro; IPR001410, DEAD.
InterPro; IPR001410, DEAD.
InterPro; IPR001296; N12N6_mtfrase.
InterPro; IPR000330; SNP2_N.
Pfam; PP00271; helicase_C.
Pfam; PP00176; SNP2_N; 1.
Pfam; PP00176; SNP2_N; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                           Helicobacteraceae; Helicobacter.
NCBI_TaxID=85963;
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STRAIN-168;
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"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAIN=A3(2) / M145;

STRAIN=23(96410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Croinin A., Fraser A., Goble A., Hidalyo J., Henrsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Ollver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SCO7673 OR SC4C2.08.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                Score 42; DB 5; Length 173; Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                         STRAIN-BIISTOL N2;
Geisel C., Stellyss L.;
"The sequence of C. elegans cosmid C08G9.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            Materston R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF036687; AAM75374.1; -
WormPep; C08G9.1; CE31155.
Hypothetical protein.
SEQUENCE 173 AA; 20056 MW; 2757D83377864CEC CRC64;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                              55.3%;
58.3%;
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Science 282:2012-2018(1998)
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Matches 7; Conservative
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Zhang J., Aronson A.I.; "A Bacillus subtills bglA gene encoding phospho-beta-glucosidase is inducible and closely linked to a NADH dehydrogenase-encoding gene.";
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                                                                                                                                                                                                                                                                Gaps
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Fuloning and sequencing of a 36-kb region of the Bacillus subtilis
genome between the gnt and iol operons.";
DNA Res. 2:61-69(1995).
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"Isolation and characterization of a hydrogen peroxide resistant mutant of Bacillus subtilis.";
Microbiology 140:297-304(1994).
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Debarbouille M.;
                                                                                                                                                                                                55.3%; Score 42; DB 16; Length 184; 54.5%; Pred. No. 26;
                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                           9E532A2748AFDE4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                          2; Mismatches
Nature 417:141-147(2002).

EMBL, AL939132; CAC17490.1; -.
InterPro; IPR065297; Lipoprotein_15.

Pfam, PF03640; Lipoprotein_15; 2.
Lipoprotein; Complete protecome.

SEQUENCE 184 AA; 19107 WW; 9E5322
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01-NOV-1996 (TrEMBLEEL. 01,
01-MAR-2002 (TrEMBLEEL. 20,
                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                   134 YNGHPLYRFAD 144
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SEQUENCE FROM N.A.
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Search completed: October 14, 2003, 08:40:16
 Caulobacter crescentus.
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SEQUENCE
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 A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Brington J., Fabret C., Ferrari E., Foulger D.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Hallo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,

RA Abdyashi Y., Koetter P., Koningstein G., Krogh S., Kumono M.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Noone D., O'Reilly M., Cogawa R., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Takeuchi M., Tamakoshi A., Taragai T., Takamashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Taramanoto H., Yanane K., Yasamotot K., Yata K.,

RA Vanida K., Wambutt R., Wedler E., Wedler H., Weitzenseyger T.,

RA Vanida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

"The complete genome sequence of the gram-positive bacterium Bacillus

"The complete genome sequence of the gram-positive bacterium Bacillus
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        Gardan R., Rapoport G., Debarbouille M.;
"Expression of the rocDEF operon involved in arginine catabolism in Bacillus subtilis.";
J. Mol. Biol. 249:843-856(1995).
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: D78193; BAA11297.1; --
EMBL: Z99124; CAB16075.1; --
                                                                                                                      Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 20, Last annotation update)
NAD-dependent epimerase/dehydratase family protein.
CC2378.
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MEDLINE=95311309; PubMed=7540694;
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                                                                                          SEQUENCE FROM N.A.
                                                                                                         STRAIN=168;
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Matches
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                                                                                                       SEQUENCE FROM N.A.
STRAIR=ATCC 19089 / CB15;
STRAIR=ATCC 19089 / CB15;
STRAIR=ATCC 19089 / CB15;
STRAIR=ATCC 19089 / CB15;
MEDLIND=21179698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shappiro L., Fraser C.M.; Proc. Matl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE=21992816; PubMed=11997336;

Bao Q., Tian Y. Li W. Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AE013002; AAM23593.1;
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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Pred. No. 49;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Lipoate-protein ligase A.
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Thermoanaerobacteriaceae; Thermoanaerobacter
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TIGRFAMs; TIGR00545; lipoyltrans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
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Job time : 21.4318 secs

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Glycine extended h
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                                                                                                    October 14, 2003, 08:34:01; Search time 52.1364 Seconds (without alignments) 94.378 Million cell updates/sec
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2: SID51/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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	Linke																									Novel human diagn	Clas I S-Locu Clas I S-rece	•	SINIS					immunogen, PO72.	ion; diagnosis; cancer; renal; bone; pe II diabetes; preeclampsia; lergy; mast cell degranulation; repair.			46 of preproadrenomedullin"	; :					
ABJ18665	AAB75113 AAB75122	AAB75123	ABJ18669 ABJ18670	AAB75124	ABJ18671	AAB75114	AAB60344	ABP72347	ABJ18668	AAB49698	AAB60345	AAE09819	AAB49699	AAB60346	ABB57209	AAB91/6/ AAB91761	AAB91765	AAW25159	ABGU5415 ABG13273	ABG09129	AAW58582	ABG14932	ABGIU4II	AAR67024	ABB62270	ABG19648	AAW56307		ALIGNMENT		1 AA.			derived imm	letection; detection; detection; dispersion; allergy; wound repair		ifiers	ues 116-1)					
4	22		.	٠,	4	2 6	10	4	4	ci c	N C	. O	10	01	m	N CN	7	a	N (101	σ,	~ ~	N M	N.	C)	~ 0	20				le; 3		5		det sase; cion; l; wo		/Qual	esid	amidated			.86	c	514. 936.
53	120	120	120	147	147	10/1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	185	206	188	188	200	185	185	184	37	25	13	229	677	775	686 6	620	10	80	1096	84 e				; peptide		st entry)	preproadrenomedullin	ntibody ed; dise regulatifunga		Location/Qualifiers	Sr note= ",	11 'note= "a			6WO-US132	2-0013	0000
0.00	0.00	0.00	0.00	0.00	0.00	0.0	0.00	0.00	0.00	6.9	200	90.B	8.0	8.0		7.0	5.8	22.0	6.1	6.1	6.13	6.5	11.0	11.3	11.3	27.3	20.7				standard;		(firs	dren	n; a elat ssion		IJ.	٠,	.m \			96	9.0	9 9 9
-		Η,			Η,	-، ا	-	-	Н																						star		161	prog	hulli od r nsmie	ens.			-site	-A1.	. 76	:96	9	95;
16	163 163	16	16	16	16	1 L	10	16	16	15	C T C	14	14	14	136	125.	123.	LO L	n un	'n	ហ	חת	51.	S	ı,	v. v.	חנח			1 1 60	AAW25160	AAW25160;	8-DEC-19	нимап рге	Adrenomedullin; antibody; detection skin; blood related; disease; type neurotransmission regulation; aller antibacterial; antifungal; wound re	Homo sapien	Key	בהרדתב	Modified-	WO9707214	7-FEB-19	6-AUG-19	- MAR-1	8-AUG-19 0-AUG-19
10	11	13	1.4 1.5	16	17	8 T F	20	21	22	233	25	26	27	28	57.00	31	32	en e	. co	36	37	30 O	0 44 0 0	41	42	43	45			RESULT AAW251			XX DT 08		KW KW KW KW						PD 27	7	-	мн

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Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20
were used for the production of anti-AM antibodies (Ab). PO70 represents
preproAM amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at
the N-terminus, PO71 represents preproAM aa 122-131 with the sequence
Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM aa

Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM ac

116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
for the prevention and/or treatment of cancers, e.g. adrenal, nervous
system, lung, colon, ovarian and breast cancer by inhibiting cell
for the prevention and therefore for treating and/or preventing diabetes
system, lung, colon, ovarian and breast cancer by inhibiting cell
glucose metabolism and therefore for treating and/or preventing diabetes
type II. They may be used for the diagnosis or treatment of conditions
creating to pregnancy e.g. preeclampsia. The Ab are also useful
for the following: (i) regulating neurotransmission or neuron growth in
areas of the central nervous system; (ii) lessening or inhibiting mast
cell degranulation and hence reducing the effects of an allergic
response, (iii) inhibiting or preventing bacterial and fungal growth (to
treat infection); (iv) facilitating wound healing; and (v) promoting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component; modification; succinimidyl, maleimido group; amino, hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                      can adrenomedullin peptide(s), Po70, Po71, Po72 and PAMP-20 - used the diagnosis and treatment of type II diabetes and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                       Martinez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 100.0%; Score 163; DB 18; Local Similarity 100.0%; Pred. No. 1.9e-18; nes 31; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adrenomedullin peptide (AM) SEQ ID NO:938.
                                     Cuttitta F, Gray K, Hook W, Macri C,
Miller MJ, Unsworth EJ, Walsh T;
            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB91762 standard; Peptide; 31 AA.
                                                                                                                                             Claim 1; Page 43; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-2000; 2000WO-US13576.
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                                                                                                                                                                                                                                                                                                                                                                                                     organ and bone development.
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                                                                             WPI; 1997-165298/15
                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA;
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10-SEP-1999;
15-OCT-1999;
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Matches
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comprising a therapeutically active amino acid region [III] and a reactive group [II] (e.g. succinimidyl and maleimido groups) attached to a leactive group [II] (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region [IV], which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. [I] are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half intracellular uptake and interference with physiological processes. ABB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                               Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; vascactive peptide; calcitonin gene related peptide; CGRP;
CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                    present invention describes a modified therapeutic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 163; DB 22;
100.0%; Pred. No. 1.9e-18;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                            Disclosure; Page 499-500; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adrenomedullin peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09827 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0070504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide receptor activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCR-) UNIV CREIGHTON.
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WPI; 2001-112059/12.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 AA;
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Gaps

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comprising a therapeutically active mathon acid region (III) and a least therapeutically active mathon acid region (III) and a least therapeutically active amino acid region (III) and a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form at peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                      Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a modified therapeutic peptide (I)
      Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 163; DB 22;
100.0%; Pred. No. 3.6e-18;
.ive 0; Mismatches 0;
100.0%; Score 163; DB 22; 100.0%; Pred. No. 3.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmes DL,
                                                                    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                       22 TVQKLAHQIYQETDKDKDNVAPRSKISPQGY 52
                                      Mismatches
                                                                                                                                                                                                                                                                                      Adrenomedullin peptide (AM) SEQ ID NO:935.
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 498; 733pp; English.
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                                    ;
                                                                                                                                                                                     AAB91759 standard; Peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                       (first entry)
                                      Conservative
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                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-1999;
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15-OCT-1999;
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                                    31;
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                        AAB91759;
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   Query Match
Best Local
                                  Matches
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AAB91759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                        Gaps
                                             The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is human adrenomedullin peptide.
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                                                                                                                                                                                                                                                                  Length 31;
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                                                                                                                                                                                                                                                                   DB 22;
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                                                                                                                                                                                                                                                                  100.0%; Score 163; DB 22; 100.0%; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                       1 TVQKLAHQIYQFTDKDKDKNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                    1 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75110 standard; Protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adrenomedullin (AM) protein.
               Column 6; 24pp; English.
                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.000
Thes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-282044/29
                                                                                                                                                                                                                                  31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-0CT-1999;
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                                                                                                                                                                                                                                  Sequence
             Claim 5;
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intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                               Length 52;
                                                                                                                                                                                                                                  1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 31; Conservative
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us-09-931-700-3.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                     The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact binding to its receptor. The present sequence is human adrenomedullin peptide.
                                                                                                                        Human; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                           Vasoactive peptides useful for inhibiting calcitonin gene related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrenomedullin; human; protein engineering; solubility; aggregation; hypotensive; vasodilator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 163; DB 22;
Pred. No. 3.6e-18;
22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                     Claim 5; Column 25-26; 24pp; English.
                                                AAE09818 standard; peptide; 52 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP55104 standard; Peptide; 52 AA.
                                                                                                     Human adrenomedullin peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                        98US-0070504
                                                                                                                                                                                                                                                          Saha S, Abel PW;
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                    peptide receptor activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adrenomedullin.
                                                                                                                                                                                                                                                                          WPI; 2001-564216/63.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AA;
                                                                                                                                                                   US6268474-B1
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                                                                                                                                                                                                                                                         Smith DD,
                                                                   AAE09818;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                               RESULT 6
                                          AAE0981
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The present sequence is that of human adrenomedullin, a potent hypotensive and vasodilator. The invention provides modified calcitonin and related peptides, such as adrenomedullin, that have at least 70% identity to the native form but are modified such that the tendency of the peptide to aggregate is reduced. Preferred regions for modification include those for which the peptide is polymorphic amongst different species, which increase the propensity of the peptide to form local interactions of the peptide so increase the net charge of the peptide. When aggregation is reduced or prevented, lower doses of the drug can aggregation is reduced or prevented, lower doses of the drug can be used. Side-effects and undesired responses are minimised by retaining high sequence identity to the human peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified human calcitonin peptide having reduced aggregation, useful for the treatment of Paget's disease, hypercalcemia and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 163; DB 24;
100.0%; Pred. No. 3.6e-18;
tive 0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                        Location/Qualifiers
16..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75111 standard; Protein; 53 AA.
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                                                                                                                                                                                                                                      17-APR-2002; 2002WO-GB01778.
                                                                                                                                                                                                                                                                                           17-APR-2001; 2001GB-0009438.
                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS INNOVATION LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                          Dobson CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-046916/04.
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les 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 AA;
                                                                         Disulfide-bond
                                                                                                                            WO200283734-A2
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis
                                                                                                                                                                                  24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                       Zurdo J,
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04-APR-2002; 2002WO-JP03374.
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                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-067581/06.
                                                                                                                    Local Similarity
Les 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AA;
                                                                                     53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABI14525
                                                                                                                                                                                                                                                                                                                                                                   WO200283907-A1
                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                      27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleavage
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                                                                                       Seguence
                                                                                                                                                                                                                                                 ABJ18665;
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Matches
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                                                                                                                                              adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment, and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                       Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                       producing
                                                                                                                                                                                                                                                                    Length
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                      Mitsushima K;
                                                                                                                                      present invention describes a method (M1) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitsushima
                                                                                                                                                                                                                                                                  Score 163; DB 22;
Pred. No. 3.7e-18;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine extended adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                            1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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                      Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 75pp; Japanese.
                                                                                                                 Example 1; Page 46; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakayama
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100.0%;
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Best Local Similarity 100.00
Local 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
(SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takimoto A, Mitsuda Y,
                      Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282044/29.
                                         2001-282044/29.
                                                                                                                                                                                                                                             53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH19808
                                                                                              recombinant host
                                                    N-PSDB; AAH19807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001
                     Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
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Pred. No. 3.7e-18;
Mismatches 0;
                                                                                                                                                                                                                                                                                           Score 163; DB 22;
Pred. No. 3.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
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                                                                                                                                                                                                                                                                                                                                                    Mismatches
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100.0%; Pre
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100.0%; Pi
tive 0;
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RESULT 11 AAB75113

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The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused
                                                                                                                                                                                                                                                                                                                    Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                            Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 163; DB 22;
100.0%; Pred. No. 9.9e-18;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 68; 75pp; Japanese.
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                                                                                                             10-OCT-2000; 2000WO-JP07023.
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                                                                                                                                                                                       (SHIO ) SHIONOGI & CO LTD
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                                                                                                                                                                                                                        Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                           WPI; 2001-282044/29.
N-PSDB; AAH19864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-282044/29.
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Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                15-0CT-1999;
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                                                                        19-APR-2001
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 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                                                                                                              Linker peptide-adrenomedullin (AM) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 163; DB 22;
Pred. No. 4.5e-18;
Mismatches 0;
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100.0%; Pred. No. *--
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                                              AAB75113 standard; Protein; 62 AA.
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Best Local Similarity 100.0
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AA;
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                                                                                                                                                                                                                                                                         Synthetic.
                                                                                     AAB75113;
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RESULT 12 AAB75122

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Length 120; Indels Length 120;

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Best Local Similarity
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Job time: 53.1364 secs
     120 AA;
                                                                                                                                                                                                                                                                Fusion peptide;
                                                                                                                                                                                                                                                                                                                          WO200283907-A1
                                                                                                                                                                                                                                                                                                   Unidentified.
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     Sequence
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                                                                                          The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for paramaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
                     Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                          Gaps
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large scale peptide production.
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                                                                                                                                                                                                                                             100.0%; Score 163; DB 22;
100.0%; Pred. No. 9.9e-18;
cive 0; Mismatches 0;
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                                                                    Claim 17; Page 69-70; 75pp; Japanese.
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                                                                                                                                                                                                                                                          Best Local Similarity
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N-PSDB; AAH19865
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                                              Gaps
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Score 163; DB 24;
Pred. No. 9.9e-18;
Mismatches 0;
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    100.08; Fr. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         large scale peptide production.
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                                           Conservative
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GenCore version 5.1.6
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- protein search, using sw model OM protein

October 14, 2003, 08:36:56; Search time 17.6136 Seconds (without alignments) 169.257 Million cell updates/sec Run on:

163 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31 US-09-931-700-3 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_76:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	adren		adrenomedullin pre		hypothetical prote	S-locus-specific g	S-locus-specific g	_	hypothetical prote	S-locus-specific g	S-locus-specific g	-locus	S-locus-specific g	probable S-recepto	ypothe	S-locus-specific g	S-locus-specific g	-locus-specific	-locus-specific	ecept	7		7	cific	cal p	probable cell divi	glycylpeptide N-te		histidine-tRNA lig
CHARACTE	ឧ	N068	S41600	10	A99638	В			G84107		T14529	T07814	Ü	ď		C86279	ď	T14423	T14416	T14530	T07809	T14528	T07812	T14418	2	9	AG0363	C134	T07810	6913
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	Length	185	188	185	189	189	430	431	373	465	428	428	429	436	857	90	427	428	428	428	429	429	431	431	434	322	328			777
ф	Query Match	100.0																	30.1			\circ	30.1	$^{\circ}$	\sim	υı	σ	σ		σ,
	Score	163	157	148	58.5	œ	58	26	54	53	52	51	51	51	51	50	20	20	49	49	49	49	49	49	49	48.5	48	48	48	48
	Result No.		7	m	4	ĸ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58

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Gaps

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ch 100.0%; Score 163; DB 2; Length 185; l. Similarity 100.0%; Pred. No. 2.3e-16; 31; Conservative 0; Mismatches 0; Indels (

Query Match Best Local Similarity Matches 31; Conserv

excinuclease ABC c	S-receptor kinase	S-receptor kinase	hypothetical prote	DNA primase (EC 2.	S-locus-specific g	flagellar M-ring p	hypothetical prote	S-receptor kinase	S-receptor kinase	transposase In4652	high density lipop	canalicular multid	UDP-3-0-[3-hydroxy	hypothetical prote	hypothetical prote
S39531	JC2482	JC2481	F71414	A55070	T14524	A84938	T33517	T14472	JQ1677	S51133	A44125	S71839	S41752	H90448	C97389
~	Н	ĸН	7	7	7	~	N	7	H	N	7	Н	7	7	7
689	856	828	1705	438	429	545	549	850	828	1004	1268	1541	340	186	204
29.4	29.4	29.4											28.5	28.2	28.2
48 29.4	48 29.4	48 29.4		47.5 29.1									46.5 28.5	١.	46 28.2

ALIGNMENTS

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A Gene: GDB:ADM
A,Cross-references: GDB:217070; OMIN:103275
A,Map position: lipter-ligter
A,Introns: 33/2; 83/2
A,Introns: 33/2; 83/2
C,Keywords: amidated carboxyl end; blood pressure control; hormone
F:12-10/Domain: signal sequence #status predicted <PIG>
F:22-10/2/Domain: signal sequence #status predicted <PIG>
F:22-10/2/Domain: proadrenomedullin #status predicted <PIG>
F:22-10/2/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PIG>
F:32-116/Product: adrenomedullin #status experimental <MAT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following F:110-115/Disulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F:116/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following F:146/Modified site: amidated Carboxyl end (Tyr) (amide in mature form from following files form from files form from following files 
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A; Molecule type: protein
A; Residues: 22-41 <KI2>
R; Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
R; Kitamura, R.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
B; Sichem. Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A; Reference number: JN0476
A; Molecule type: protein
A; Residues: 95-146 <KI3>
A; Residues: 95-146 <KI3>
A; Residues: 95-146 <KI3>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-185 <1SH>
A;Residues: 1-185 <1SH>
A;Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem: Biophys, Res. Commun. 134, 720-725, 1993
A;Fitle: Cloning and characterization of EDNA encoding a precursor for human adrenome
A;Reference number: JN0684; MUID:93343928; PMID:7688224
                                                                C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-7eb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-7eb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2351; JN0664; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, Biochen. Blophys. Res. Commun. 23, 631-639, 1994
Biochen. Blophys. Res. Commun. 23, 631-639, 1994
A;Itile: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869; PMID:8074714
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adrenomedullin precursor - human
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A; Residues: 1-185 <KIT>
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R. Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A.;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A.;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D85212; NID:92351155; PIDN:BAA21946.1; PID:92351156
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein 20078 [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                          A;Cross-references: GB:BA000007; PIDN:BAB33496.1; PID:913359529; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Escherichia coli
C;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 14-Sep-2001
C;Accession: A85489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 189;
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A; Accession: T14536
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34.4%; Pred. No. v...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%; Score 58.5; Dilarity 34.4%; Pred. No. 0.5; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
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C;Superfamily: Escherichia coli yabP protein
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C,Superfamily: Escherichia coli yabP protein
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A;Molecule type: DNA
A;Residues: 1-189 <STO>
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Best Local Similarity
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-189 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                          hypothetical protein ECs0073 [imported] - Escherichia coli (strain 0157:H7, substrain RI C;Species: Escherichia coli ("Species: Escherichia coli ("Species: B-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 ("Accession: A99638 "R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 1.8e-15;
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Pred. No. 3.7e-14;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                    TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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Best Local Similarity 87.1%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-188 <KIT>
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Matches 30; Conserv
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A; Molecule type: DNA
A; Residues: 1-465 <DN2
A; Cross-references: EMBL:U41279; NID:91086905; PID:91086919; PIDN:AAB52685.1; GSPDB:G
A; Experimental source: strain Bristol N2; clone C17C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                714529
S-locus-specific glycoprotein - wild cabbage (fragment)
S-locus-specific glycoprotein
C;Alecrade names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14529
R;Kusaba, M; Nishio, T; Satta, Y; Hinata, K; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D85205; NID:92351141; PIDN:BAA21939.1; PID:92351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
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C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
F;32-426/Domain: S-locus-specific glycoprotein homology <SSG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Raphanus sativus (radish)
C.Species: Raphanus sativus (radish)
C.Species: Raphanus sativus (radish)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C.Accession: TOT814
R.Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A.Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus re A.Reference number: 216146; MUID:98311079; PMID:9648745
A.Accession: T07814
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-428 <SAK>
A.Residues: 1-428 <SAK>
A.Conetics: EMBL:AB009682; NID:93327849; PIDN:BAA31729.1; PID:93327850
C.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                           Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 2; Length 428
Pred. No. 11;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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A;Reference number: 218078; MUID:97352858; PMID:9207151
A;Accession: T14529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <KUS>
  submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid C17C3.
A; Reference number: Z18366
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                                                                                                                                                                                                                                                                                                                                                                           DB 2;
8.7;
                                                                               A; Accession: T15540
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                       A; Introns: 124/2; 138/2; 174/2; 223/1; 369/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 QEIAHKFEDFTELKKDSFSP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 OKLAHQIYQFTDKDKDNVAP 22
                                                                                                                                                                                                                                                                                                                                                                        32.5%;
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28.2%;
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les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                                                                                                                A; Gene: CESP:C17C3.1
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Best Local S
Matches 8
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                                                                                                                                                                                                                                             C; Genetics:
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Matches
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                                                                                                                                                                                                                                                                                                                 N,Alternate names: $ glycoprotein
C,Species: Brashica rapa (turnip)
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C,Accession: T14415
K,Rusaha, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A,Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uppolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C; Accession. G84107 R; Takani, H.; Nakasone, K.; Takani, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132 A; Accession: G84107 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07382.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: DNA
A; Residues: 1-431 <KUS-)
A; Cross-references: EMBL: D85215; NID: 92351161; PIDN: BAA21949.1; PID: 92351162
A; Cross-references: EMBL: D85215; NID: 92351161; PIDN: BAA21949.1; PID: 92351162
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: 91ycoprotein
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 *sequence_revision 20-Sep-1999 *text_change 20-Sep-1999
C;Accession: T15540
R;Du, 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Length 430;
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                                                         Indels
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                                                                                                                                                           230 EKLSYMVYNFTENNEEVAYTFRMTNNSIYSRLTVSPEGY 268
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                                                                                                          3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 218078; MUID:97352858; PMID:9207151
A; Accession: T14415
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                      7;
        2;
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Pred. No. 2.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
4.9;
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                                                   12; Mismatches
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     Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54;
Pred. No.
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     35.6%;
25.6%;
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ilarity 30.8%;
Conservative
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                                                      10; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 12; Conserv
     Query Match
Best Local Similarity
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A; Residues: 1-373 <STO>
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                                                         Matches
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          Plant J. 6, 807-813, 1994
A;Title: Expression of the S-locus receptor kinase multigene family in Brassica olera A;Reference number: 218108; MUID:95152555; PMID:7849754
A;Accession: T14471
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: implicated in the self-incompatibility system of Brassica oleracea C; Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal F; 41-436/Domain: S-locus-specific glycoprotein homology <SSG>
F; 526-813/Domain: protein kinase homology <KIN>
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A; Realdues: 1-90 <STO>
A: Cross-references: GB: AE005172; NID: 97262688; PIDN: AAF43946.1; GSPDB:GN00141
C; Genetics:
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A; Residues: 1-857 < KUN>
A; Cross-references: EMBL: Z30211; NID: 9459244; PIDN: CAA82930.1; PID: 9459245
A; Experimental source: strain alboglabra; stigma
A; Genetics:
A; Gene: Six29
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8; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 438/1; 481/1; 544/3; 615/1; 694/2; 744/3
C; Function:
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Pred. No. 3
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Best Local Similarity 28.2%;
Matches 11; Conservative
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R; Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A; Title: Striking sequence similarity in inter- and intra-specific comparisons of class
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C; Species: Brassica oleracea (wild cabbage)
C; Species: Brassica oleracea (wild cabbage)
C; Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
C; Accession: A27827
R; Nasrallah, J.B.; Kao, T.H.; Chen, C.H.; Goldberg, M.L.; Nasrallah, M.E.
R*Initie: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus A: Reference number: A93392
A; Reference number: A3332
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-436 ANAS>
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Superfamily: S-locus-specific glycoprotein S6 #status predicted ANAI>
F; 1-31/Domain: signal sequence #status predicted ASGS>
F; 40-434/Domain: S-locus-specific glycoprotein homology SSGS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: 218078; MUID:97352856; PMID:9207151
A;Accession: T14533
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-429 <KUS>
A;Cross-references: EMBL:D85209; NID:92351149; PIDN:BAA21943.1; PID:92351150
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable S-receptor kinase (EC 2.7.1.-) srk29 - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                10;
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              Length 428;
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16;
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                                                                            Indels
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                                                                         10;
              DB 2;
          Score 51; DB;
Pred. No. 16;
B; Mismatches
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R; Kumar, V.; Trick,
Query Match
Best Local Simi
Matches 11;
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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2003, 08:35:36; Search time 9.86364 Seconds (without alignments) 147.798 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-931-700-3 163 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	ADML_HUMAN	ADML_PIG	ADML_CANFA	ADML_RAT	ADML_BOVIN	ADML_MOUSE	ILVD_BIFLO	SLS6_BRAOL	VG48_BPMU	SLS2_BRAOA	Y4KA_RHISN	ZIPA_YERPE	SYH_METTH	NMT1_HUMAN	NMT1_MOUSE	NMT1_BOVIN	UVRA_PSELE	PRI1_DROME	FLIF_BUCAI	VGLN_HUMAN	MRP2_RAT	LPXD_YEREN	DNAB_RHOMR	SLS3_BRAOL	SPAC_BACSU		MIG6_MOUSE	YKF0_YEAST	MRP2_HUMAN	PKSK_BACSU	- 1	MIG6_RAT	SYPC_YEAST
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FRDA_HAEIN CC47 YEAST	MYSJ_DICDI YBA4_YEAST	FAF_DROME	MY15_HUMAN GCS3_SULTO	YK96_AERPE LAC1_AGABI	LAC2_AGABI COAT_SMSV4
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                                                                                                                                                                                                                                                        -I-FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMESTAGES. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN PITITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                        MEDITINE=20053666; PubMed=10588445;
Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
Structure-activity relationships of adrenomedullin in the circulation
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
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AMIDATION (G-147 PROVIDE AMIDE GROUP).
                                    Matsuo H., Eto T.; "Adrenomedullin: a novel hypotensive peptide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hormone; Amidation; Cleavage on pair of basic residues; Signal;
            MEDLINE-93249425; PubMed-8387282;
Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREPROAM C-TERMINAL FRAGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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                                                              pheochromocytoma.";
Biochem. Biophys. Res. Commun. 192:553-560(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADRENOMEDULLIN
                                                                                                                                     "Proadremomedullin-derived peptides.";
Front. Neuroendocrinol. 19:100-127(1998).
                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D43639; BAA07756.1; ALT_SEQ.
                                                                                                              MEDLINE=98240137; PubMed=9578982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D14874; BAA03589.1; -. EMBL; S73906; AAC60642.1; -.
                                                                                                                                                                                                                               and adrenal gland.";
Regul. Pept. 85:1-8(1999).
TISSUE=Pheochromocytoma;
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                                                                                                                             Samson W.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T., "Complete amino acid sequence of porcine adrenomedullin and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEGUENCE OF 22-41.

TISSUB-Adrenal medulla;

MEDLINE-94357274; PubMed-8076689;

Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,

Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,

Rawamoto M., Minamino N., Matsuo H., Eto T.;

"Identification and hypotensive activity of proadrenomedullin

"Top opetide (PAMP).";

FEBS Lett. 351:35-37(1994).

"I FINCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP).
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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                                                                                                      Length 185;
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PREPROAM C-TERMINAL FRAGMENT
                                                                                                                                                         Indels
S -> R (in dbSNP:5005).
/FTId=VAR_014861.
64C7D2A0B4654DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                           100.0%; Score 163; DB 1; 100.0%; Pred. No. 4.2e-16;
                                                                                                                                                                                                                              116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                     188 AA
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                                                                                                                                                   0; Mismatches
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PIR; S41600; S41600.
InterPro; IPR001710; Adrenomedullin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Adrenal medulla;
MEDLINE=94139945; PubMed=8043068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of cDNA encoding its precursor."; FEBS Lett, 338:306-310(1994).
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                                                185 AA; 20420 MW;
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                                                                                                                           Local Similarity
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                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99002704; PubMed=9788655;
Ono Y., Kojima M., Okada K., Kangawa K.;
"cDNa Cloning of canine adrenomedullin and its gene expression in the
mart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 BY SIMILARITY.
PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                         Gaps
                                                                                                                                                                                                                                                                           Proadrenomedullin N-20
                                                                                                                                                                                                               077559; Q9TVC9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2C
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
AMIDATION (G-147 PROVIDE AMIDE GROUP). 71749460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-147 PROVIDE AMIDE GROUP)
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BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 188;
                                          Length 188;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Imoto I., Jougasaki M.;
"Cloning of cDNA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> K (IN REF. 2).
809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 152; DB 1;
Pred. No. 1.6e-14;
                                           DB 1;
                                           Score 157; DB 1
Pred. No. 3e-15;
                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENOMEDULLIN
                                                                                                                                                                                                     188 AA.
                                                                                                   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U96127; AAD09957.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                     PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF045773; AAD05423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00801; ADRENOMEDULN.
             20893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.3%;
                                          96.38;
96.88;
                                                                        30; Conservative
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
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 146
188 AA;
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Best Local Similarity
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                                                         Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9615;
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                                                                                                                                                                                                     ADML_CANFA
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                SEQUENCE
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                                             Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-96102137; PubMed-8524787; Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N., Sulpizio A.C., Aiyar N.V., Ruffold R.R. Jr., Feuerstein G.Z., Biscovery of adrenomedullin in rat ischemic cortex and evidence for "Discovery of adrenomedullin in rat ischemic damage."; its role in exacerbating focal brain ischemic damage."; Proc. Natl. Acad. Sci. U.S. A. 92.11480-11484(1995).
-- FUNCIION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASOBILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and biological activities of rat adrenomedullin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-i- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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AMIDATION (G-144 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREPROAM C-TERMINAL FRAGMENT
Indels
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35CAD9A9DD19AE35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley, TISSUE-Adrenal gland, MEDLINE-93384621; PubMed-7690563;
                                                                 TVQKLAHQIYQFTDNDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN
                                                                                                                                                             185 AA.
                                 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20636 MW;
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29; Conservative
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue-Brain;
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ADML_MOUSE
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                                             Gaps
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16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barker S., Wood E., Clark A.T.L., Corder R.;
"Cloning of bovine preproadrenomedullin and inhibition of its basal
Life Sci. 62:1407-1415(1988).
-!-PUNCTION: HYPOTENSTYE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CIRCULATION CONTROL (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).

AMIDATION (G-147 PROVIDE AMIDE GROUP)
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AMIDATION (G-42 PROVIDE AMIDE GROUP)
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        Length 185;
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                                           1; Indels
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  Score 148; DB 1;
Pred. No. 5.7e-14;
; Mismatches 1;
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                                                                                                     1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                        188 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98244567; PubMed=9585168;
                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
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90.8%;
87.1%;
                                     27; Conservative
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                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                         taurus (Bovine)
                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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les 28; Conserv
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                                                                                                                                                                                                             ADML_BOVIN
062827;
  Query Match
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PEPTIDE
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                                                                                                                                                                                                 ADML BOVIN
                                       Matches
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Matches
                                                                                                                                                                          RESULT 5
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PRT; 184 AA.
P97297; P97453;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of adrenomedullin, a hypotensive peptide, in the trophoblast giant cells at the embryo implantation site in mouse."; Dev. Biol. 203:264-275(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; "Genomic organization, expression, and chromosomal mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99046755; PubMed-9808778;
Yotsumoto S., Shimada T., Cul C.Y., Nakashima H., Fujiwara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 184;
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C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDUIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      !- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                        STRAIN-129/Sv;
MEDLINE-97092892; PubMed-8938454;
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse adrenomedullin gene.";
Genomics 37:395-399(1996).
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83.9%;
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nes 26; Conservative
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184
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InterPro; IPR001710;
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-2294977; PubMed-12381787; Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.; "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal ract." Tact.", Froc. Natl. Acad. Sci. US., 99:14422-14427(2002).

-I. CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea (Cauliflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00886; ILVD_EDD_1; 1.
PROSITE; PS00887; ILVD_EDD_2; FALSE_NEG.
Branched-chain amino acid biosynthesis; Lyase; Iron; Iron-sulfur;
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č
                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
463F654306027A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
-1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
-1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 620;
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01-AUG-1990 (Rel. 15, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                                                                            15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
11hydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
ILVD OR BL1788.
                                                                                 620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 12;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 VVKIAHQYY---DDSDDSVLPRSIATKEAF 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002691; ILVD EDD family; 1.
TIGRFAMS; TIGR00110; 11VD; 1.
                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE014813; AAN25571.1; -.
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Pfam; PF00920; ILVD_EDD; 1.
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Matches 12; Conservative
                                                                                    STANDARD;
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                                                                                                                                                                                                                                                     Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NCC 2705
                                                                                 LVD BIFLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ature 320:323-323(1987).

:- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
                                                                        SEQUENCE FROM N.A.
Nasrallah J.B., Kao I.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.;
"Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of Brassica oferacea.";
                                                                                                                                                                                                                                                                      Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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M-LINKED (GLCNAC. .) (POTENTIAL).
M, E2332635B885A515 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN B.OLERACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
Nature 326:523-523(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Polymorphism; Signal.
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eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last sequence update)
Protein gp48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A27827; A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR0010589; Pan_app.
InterPro; IPR000569; Slocus_glycop.
Pfam; PF01453; Agglutinin; 1.
SMART; SM00108; B_lectin, 1.
SMART; SM00108; Plectin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X00268; CAA68375.1; -. EMBL; X03170; CAA26934.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: STIGMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINASE RECEPTOR (ZMPK1).
                                                                                                                                                                                                                                               SEQUENCE OF 22-435 FROM N.A.
                                                                                                                                                                                          Nature 326:617-619(1987).
                                                                                                                                                                                                                                                                                                                                                              Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Self-incompatibility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                          NCBI_TaxID-3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VG48_BPMU
Q9T1V1;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                      oleracea.
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CHAIN
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               DOR NO DO
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                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                             Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO H.INFLUENZAE H11521 AND SOME, TO E.COLI YMFQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea var. alboglabra (Chinese kale).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A homozygous S genotype of Brassica oleracea expresses two S-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- TISSUE SPECIFICITY: STIGMA.
-I- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN B.OLERACEA.
                          Bacteriophage Mu.
Viruses; dsDAH viruses, no RNA stage; Caudovirales; Myoviridae;
Mu-like viruses.
                                                                                                                                                 SEQUENCE FROM N.A.
Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Haemophilus influenzae Mu-like prophage FluMu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01126.1; -.
20468 MW; 3045A6C185B48BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
5-locus-specific glycoprotein BS29-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Genet. 218:112-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89384424; Pubmed=2550759;
Trick M., Flavell R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S04906; S04906.
InterPro; IPR001480; B_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 KPAHQIYKEVYHDGDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KLAHQIYQFTDKDKDN 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF083977; AAF01126.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINASE RECEPTOR (ZMPK1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.58
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 AA;
                                                                                                    NCBI_TaxID=10677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SLS2_BRAOA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97305956; PubMed-9163424;
Fretberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                    S-LOCUS-SPECIFIC GLYCOPROTEIN BS29-2.
N-LINKED (GLONAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of symbiosis between Rhizoblum and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                   30.1%; Score 49; DB 1; Length 435;
                                                                                                                                         Self-incompatibility; Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Plasmid.
SEQUENCE 322 AA; 36690 MW; 177B0AF61FA0C74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 OKLSYMVYNFTONSEEVAYTFIMTNNSIYSRLTISSSGY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 AA
                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 18;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 VNKLADEI-QFTTKNSFSATPSAELDPANH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence
01-NOV-1997 (Rel. 35, Last annotation
Hypothetical 36.7 kDa protein Y4KA.
InterPro; IPR003609; Pan_app.
InterPro; IPR000858; Slocus_glycop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                 Pfam; PF01453; Agglutinin; 1.74
Pfam; PF00954; S.Jocus_glycop; 1.
SMART; SM0108; B_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                      49543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium sp. (strain NGR234).
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 11; Conservative
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120
244
260
389
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                                                                                                                                                                                                           113
120
244
260
389
435 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
Les 11; Conserv
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P55521;
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P58492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perret X.;
                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINB-22137865; PubMed-12142430;
MEDLINB-22137865; PubMed-12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 184:4601-4611(2002).

-1- FUNCTION: Interacts directly with the cell division protein ftsz.

Probable receptor for the septal ring structure, may anchor it to the inner-membrane (By similarity).

-1- SUBCELLULAR LOCATION: Type ID membrane protein. Inner membrane (By
                                                                                                                                                                      MEDLINE-21470413; PubMed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                        Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP, MF_00509; -; 1.
Pfam; PF04354; ZipA_C; 1.
Cell division; Septation; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL CYTOPLASMIC (POTENTIAL) EA04B89084649044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERIPLASMIC (POTENTIAL).
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
c28-FEB-2003 (Rel. 41, Last annotation update)
ZIPA OR YPO2990 OR Y1491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- SIMILARITY: Belongs to the zipA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 VEKPAHOVAPQQHVESQQEPVAPAPEAKPQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Yersinia pestis KIM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VQKLAHQI--YQFTDKDKDNVAPRSKISPQ 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.4%; Score 48; 36.7%; Pred. No. ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ414154; CAC92234.1; -.
EMBL; AE013752; AAM85062.1; ALT_INIT.
                                                                                                                                                               / Biovar Orientalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 C
36098 MW;
                                                                                                    Enterobacteriaceae; Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 36.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; AG0363; AG0363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                              SEQUENCE FROM N.A.
                                                                           Yersinia pestis.
                                                                                                                     NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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    δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Mang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glycylpeptide N-tetradecancyltransferase 1 (EC 2.3.1.97) (Peptide N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase)
1) (NMT 1) (Type I N-myristoyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50862; AA_TRNA_LIGASE_II; 1. Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
15.JUL-1998 (Rel. 36, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                        Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1; Length 425; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AA; 48019 MW; 8388A5975A017535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 EEVVNQIYHFTDKGGRELALRPBLT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QKLAHQIYQFTDKDKDNVAPRSKIS 27
                                                                                                                                                            Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000811; AAB84750.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004516; Hiss.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR006195; tRNA_ligase_II.
                                                                                                                                                                                                                                                                                                                         STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03129; HGTP_anticodon; 1. Pfam; PF00587; tRNA-synt_2b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIGRFAMS; TIGRO0442; hiss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome SEQUENCE 425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; 032422; 1Q
HAMAP; MF_00127;
                                                                                                                                      HISS OR MTH244.
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425 AA.

PRT;

STANDARD;

SYH_METTH 026346;

RESULT 13 SYH_METTH

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NMT1_MOUSE
070310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM;
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           SO PRESENTANTA PROPERTY OF SO PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RADINE-2338257; PubMed-12477932;

REAL Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,

RA Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Richards S.A., McEwan P.J., McKernan M.J., Madan A.M., Gab L.J., Hulyk S.W.,

RA Richards S., Worley D.M., Schergren E.J., Lu X., Gibbs R.A.,

RA Hilalon D.K., Munny D.M., Scheuren E.J., Lu X., Gibbs R.A.,

RA Hotiquez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Blakesley R.W., Touchman J.W., Scheure E.D., Dickson M.C.,

RA Schheroth A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand Maria M.A., Schein J.E., Short R.M.,

Rand Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand Maria M.A., Schein J.E., Short R.M.,

Rand Maria M.A., Schein J.E., Short R.M.,

Rand M. Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand M. Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand M. Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand M. Maria M.A., Schein J.E., Jones S.J.M., Maria M.A.;

Rand M. Maria M.A., Schein J.E., Short M. Maria M.A.;

Rand M. Maria M.A., Schein J.E., Short M. Short L. L. Short J. Schein J.E., Short M. Short L. Short J. Schein J.E., Short M. Short J. Schein J.E., Short M. Short J. Short M. Short J. Short M. Short J. Short M. Sho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blockem, J. 333:491-495(1998).
-!- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue of certain cellular and viral proteins.
-!- CATALITIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-
                                                                                                                                          SECUENCE OF 58-496 FROM N.A., AND MUTAGENESIS OF GLY-492.
MEDLINE=92237320; PubMed=1570339;
Duronio R.J., Reed S.I., Gordon J.I.;
"Mutations of human myristory."Coo.protein N-myristoryltransferase
cause temperature-sensitive myristic acid auxotrophy in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-myristoyltransferase: evidence for an alternative splice variant of the enzyme.";
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glover C.J., Hartman K.D., Felsted R.L.; Human N.myristcoyltransferase amino-terminal domain involved in targeting the enzyme to the ribosomal subcellular fraction."; J. Biol. Chem. 272:28680-28689(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA -!- SIMILARITY: BELONGS TO THE NAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Characterization of human and rat brain myristoyl-CoA:protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 81-89 FROM N.A.
MEDLINE-98343933; PubMed-9677304;
Mcilhinney R.A.J., Young K., Egerton M., Camble R., White A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                     cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A second mammalian N-myristoyltransferase.";
J. Biol. Chem. 273:6595-6598(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P30419-2; Sequence=VSP_003570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P30419-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98019247; PubMed-9353336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98175914; PubMed=9506952; Glang D.K., Cravatt B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tetradecanoylglycyl-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name-Short;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soloviev M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Η;
Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
61yCylpeptide N-tetradecancyltransferase 1 (EC 2.3.1.97) (Peptide N-myristcyltransferase 1) (Myristcyl-CoA:protein N-myristcyltransferase 1) (Myristcyl-CoA:protein N-myristcyltransferase 1) (Myristcyl-CoA:protein N-myristcyltransferase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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G->D,K: REDUCED ACTIVITY.
7661140D3837BE7A CRC64;
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PROSITE; PS00976; NWT 2: 1.
Transferase; Acyltransferase; Alternative splicing.
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J. Biol. Chem. 273:6595-6598(1998).
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Pred. No. 29;
7; Mismatches
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                                                                                                                                                                                                          EMBL; M86707; -; NOT_ANNOTATED_CDS.
EMBL; AF043324; AAC09294 1; ALT_INIT.
EMBL; AF020500; AAB95316.1; -.
EMBL; BC00658; AAH06538.1; -.
EMBL; BC00558; AAH06569.1; -.
EMBL; BC007258; AAH06569.1; -.
EMBL; BC008112; AAH08312.1; -.
EMBL; RC008112; AAH08312.1; -.
EMBL; RC008112; AAH08312.1; -.
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Pfam; PF01233; NMT; 1.
Pfam; PF02799; NMT_C; 1.
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA BOSAK S.A., McEwan P.J., Wokeran K.J., Amalek J.A., Gunartan P.H.,
RA HOLLING S., Wollard K.C., McEwan R.J., Lu X., Gubra R.M.,
RA Holling M. Madan A., Young A.C., Shevchenko Y., Dunifard G.G.,
RA Pahoy J., Helton E., Kettenma M., Madan A., Rodigues S., Sanchez A.,
Rahoy J., Helton E., Kettenma M., Madan A., Rodigues S., Sanchez A.,
Rahoy J., Helton E., Kettenma M., Madan A., Rodigues S., Sanchez A.,
Rahoy J., Helton E., Kettenma M., Wadan A., Rodigues S., Sanchez A.,
Rahotiguez A.C., Gilmood J., Schmitz J., Myers R.M.
Rahotiguez C.D.
Rahotiguez G.D.
Rahotiguez G.J.
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Search completed: October 14, 2003, 08:39:11 Job time: 11.8636 secs

108 TMEEASKRSYQFWDIQPVPKLGEVVNTHGPVEPDKDNIRQEPYTLPQGF 156

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Q8xa03 escherichia
Q8xa03 escherichia
Q9seb5 hirschfeldi
023849 brassica ca
0285p2 raphanus ra
Q8sb2 brassica ol
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Q9trz6 sus scrofa
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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163
1 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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RESULT 2 Q9TRZ6 ID Q9TRZ6 Pred. No. 1.6;

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MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Hayasin T., Makfino K., Ohnishi M., Kurokawa K., Ishili K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Rohara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-21074935; Pubmed*11206551;
Perna N.T., Plunkett G. III, Burlind V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
ADRENOMEDULIN.
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Pred. No. 5.2e-13;
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EMBL; AP002550; BAB33496.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLEEL 20, 01-MAR-2002 (TrEMBLEEL 20, 01-MAR-2002 (TrEMBLEEL 20, HYPOTHEICAL protein 20078, 20078 OR ECS0073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                       NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8XA03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
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ACCOCCOS DE LA COCCOS DEL COCCOS DE LA COCCOS DEL COCCOS DE LA COCCOS DELA COCCOS DE LA COCCOS DE LA COCCOS DE LA COCCOS DE LA COCCOS D
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DB 16; Length 189;

Score 58.5;

35.9%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97352858; PubMed=9207151;
Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
Striking sequence similarity in inter- and intra-specific comparisons of class I SLG alleles from Brassica oleracea and Brassica campestris: Implications for the evolution and recognition mechanism.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pistil;
MEDLINE-21148766; PubMed-11254120;
Luu D.T., Hugues S., Passelegue E., Heizmann P.;
"Evidence for orthologous S-locus-related I genes in several genera of
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Durschfeldia incana.
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Hirschfeldia.
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.6%; Score 58; DB 10; Length 430; 25.6%; Pred. No. 4.6; Live 12; Mismatches 7; Indels 1
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 AA; 49149 MW; E76EC9219F8D9641 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).

BMBL: D85212; BAA21946.1; -.

InterPro: IPR001400; B_lectin.

InterPro: IPR003014; PAN.

InterPro: IPR003014; PAN.

InterPro: IPR003069; Pan.app.

InterPro: IPR003609; Slocus_glycop.

Pfam; PP010453, Agglutinin; 1.

Pfam; PP00044; PAN: 1.

Pfam; PP00108; B_lectin; 1.

SWART; SW00108; B_lectin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||:::|||:::|| 330 EKLSYMVYNFTENNEEVAXTFRMTNNSIYSRLTVSPEGY 268
                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
S glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 QKLAHQIYQFTDKDKD-----NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
S-locus related (Fragment).
  7;
                                                                   4 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 30
                                                                                                                                                                                                   430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AA.
  9; Mismatches
                                                                                                                                                                                                     PRI;
                                                                                                                                                                                                                                                                                                                                 Brassica oleracea (Cauliflower).
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3712;
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SEQUENCE
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Luu D.T., Hugues S., Passelegue E., Heizmann P.;
"Evidence for orthologous S-locus-related I genes in several genera of
  Raphanus raphanistrum subsp. raphanistrum.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                              368 AA; 41672 MW; 1D455F6FB9B704D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                    3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                     33.7%; Score 55; DB 10; 28.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA
                                                                                                                                                                                                                                                                                                  ; Pred. No. 11;
10; Mismatches
                                                                                                                                                                      Interpro: IPR001480; B_lectin.
Interpro: IPR001858; Slocus_glycop.
Pfam: PF01453; Agglutinin; 1.
SMAR; SM00108; B_lectin; 1.
                                                                                                                                                  Mol. Gen. Genet. 264:735-745(2001).
EMBL: AF162905; AAF22264.1; -
                                                                                      TISSUE-Pistil;
MEDLINE-21148766; PubMed=11254120;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea (Cauliflower),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QKLAHQIYQFTDKDKD---
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Tocal 12; Conserva'
                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 11; Conserv
                                                                          SEQUENCE FROM N.A.
                                       eurosids II; Brass.
NCBI_TaxID=109997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Kinase.
                                                                                                                                      Brassicaceae.";
                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                     Query Match
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                            08S9B2
   Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97352858; PubMed-9207151;
Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
"Striking sequence similarity in inter- and intra-specific comparisons
of class I SLG alleles from Brassica oleracea and Brassica
campestris: Implications for the evolution and recognition
mechanism.";
                                                                                                                                                                                                                                                                                                                                                    Brassica campestris (Field mustard).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.

NCBI_TaxID=3711;
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                             Score 56; DB 10; Length 367;
Pred. No. 7.6;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 431;
                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                      367 AA; 41676 MW; 48943E2EA85A2E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49227 MW; BED2FAFB8C3CD4B5 CRC64;
                                                                                                                                                                                                            3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                    01-57N-1998 (TrEMBLrel. 05, Created)
01-5AN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QKLAHQIYQFTDKDKD-----NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).

BMBL: D85215; BAA21949.1; -.

InterPro: IPR001440; Blectin.

InterPro: IPR003609; Pan.app.

InterPro: IPR00868; Slocus_glycop.

Pfam; PF001453; Agglutthin; 1.

SMART; SM00108; B_lectin; 1.

SMART; SM00473; PAN.Ap; 1.
                                                                                                                                                                                                                                                                                  431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.4%; Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
     MOI. Gen. Genet. 264:735-745(2001).
EMBL: AF162909; AAF22268.1;
InterPro; IPR001480; B_lectin.
InterPro; IPR000858; Slocus.glycop.
Pfam; PF01453; Agglutinin; 1.
Pfam; PF00954; S_locus.glycop.
SMART; SM00108; B_lectin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                              34.4%;
28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, S-locus related (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%;
                                                                                                                                                                                                                                                                                                                                           S glycoprotein (Fragment).
                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.8 Matches 12; Conservative
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                           367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 AA;
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                          367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431
Brassicaceae.";
                                                                                                                    SEQUENCE
                                                                                             NON_TER
NON_TER
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
NON_TER
                                                                                                                                                                                                                                                                                             023849;
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                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                       RESULT 6
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Gaps

10;

Length 368;

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A Kimura R., Sato K., Fujimoto R., Nishio T.;

A Kimura R., Sato K., Fujimoto R., Nishio T.;

A Kimura R., Sato K., Fujimoto R., Nishio T.;

Targenition specificity of self-incompatibility maintained after the divergence of Brassica oleracea and Brassica rapa.";

Submitted (AGG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, ABO70624; BaB86338.1;

DR InterPro: IPR001480; Balectin.

DR InterPro: IPR003094; Pan.

BR InterPro: IPR003094; Pan.

DR Ffam, PF001453; Agglutinin; 1.

PR Pfam, PF00024; PAN; 1.

DR Pfam; PF00184; S. locus_glycop; 1.

BR Ffam; PF00108; B_lectin; 1.

BR SMART; SM00108; B_lectin; 1.
                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.7%; Score 55; DB 10; Length 421; 30.8%; Pred. No. 12; tive 8; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AA; 48015 MW; 835E29608FC9F160 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NVAPRSKISPQGY 31
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                               32.5%; Score 53; DB 5; Length 346; 40.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 5; Length 357;
Pred. No. 20;
7; Mismatches 5; Indels
                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Du Z.;
"The sequence of C. elegans cosmid C17C3.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       346 AA; 39688 MW; CF853F9CAF0B93B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41046 MW; D62561FC872C1158 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 41.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                             357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 AA.
                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                           WormPep; C17C3.1b; CE27071.
InterPro; IRR003703, Acyl_CoA_thio.
Pfam; PF02551; Acyl_CoA_thio; 2.
IIGRFAMS; TIGR00189; tesB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; C1703.1a; CE27070.
InterPro; IPR003703; Acyl_Coa_thio.
Pfam; PF02551; Acyl_Coa_thio; 2.
TIGRNAMS; TIGR00189; tesB; 1.
BYPOTHACICAL protein.
SEQUENCE 357 AA; 41046 MW; D6251
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                               37 QEIAHKFFDFTELKKDSFSP 56
                                                                                                                                                                                                                                                       3 QKLAHQIYQFTDKDKDNVAP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QKLAHQIYQFTDKDKDNVAP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 QEIAHKFFDFTELKKDSFSP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Direct Submission.";
Submitted (SEP-2001) to the E
EMBL: U41279; AAK31428.1; -.
HSSP; P23911; 1C8U.
     EMBL; U41279; AAK31429.1; -.
HSSP; P23911; 1C8U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.00,
Best Local 8; Conservative
                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                       Hypothetical protein.
                                                                                                                                                                                             Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                                                                                                               Query Match
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Q8H0C3;
                                                                                                                                                                                                                                                                                                                                                                                                               Q9BIA9;
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ID 06
AC 06
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                                                                                                                                                                                                                                                                                                                   STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takani H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
halodurans and genomic sequence comparison with Bacillus subtilis.";
halodurans and genomic sequence Library 1.
Interpreto; IPR001296; Glyco_trans=1.
Fifen; PF00534; Glyco_trans=1.
Ffan; PF00534; Glyco_trans=1.
Ffan; PF00534; Glyco_trans=1.
Ffan; PF00534; Glyco_trans=1.
Ffan; PF00F0534; Glyco_trans=1.
Ffan; PF00F0534; Glyco_trans=1.
Ffan; PF00F0534; Glyco_trans=1.
Ffan; PF00F0534; Glyco_trans=1.
Ffan; FF00F0534; Glyco_trans=1.
Ffan; FF00F0534; Glyco_trans=1.
Ffan; FF00F0534; Glyco_trans=1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis,
NCBI_TaxID=6239;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.1%; Score 54; DB 16; Length 373;
48.0%; Pred. No. 15;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmioutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans cosmid C17C3.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
227 QKLSYMMYNFTDNSEEVAYTFLMTNNSFYSRLKLSSEGY 265
                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBirel. 17, Created)
01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-MRR-2003 (TrEMBirel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VQKLAHQIYQFTDKDKDNVAPRSKI 26
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                       Lipopolysaccharide biosynthesis.
BH3663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 39.7 kDa protein. C17C3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.08
Matches 12; Conservative
                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.; "Direct Submission.";
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                                                                                                               Q9K6R4;
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                                                                                             Q9K6R4
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PRELIMINARY;
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                                  01-JUN-1998
                                            01-JUN-1998
01-JUN-2001
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Best Local S
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                                                                                                         Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8L163
Q8L163;
         056958
                       056958
                                                                                                                                                                                                               URR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Brāssicā oleracēa (čauliflower).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                     DB 10; Length 430; 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                            9; Indels
                                                                                                                          SEQUENCE FROM N.A. Odashina M., Okamoto S., Nishio T.; Odashina M., Okamoto S., Nishio T.; Distribution of S haplotypes in Brassica napus."; Submitted (200-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB086974; BAC57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48724 MW; 18E04542C7293BEA CRC64;
                                                                                                                                                                                                              430 AA; 49065 MW; 60152ED337CD0928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKLSYMVYNFTENSEEVAYTFRMTNNSFYSRLKVSSDGY 267
                                                                                                                                                                                                                                                                                                   230 QKLGYMVYNFTENSEEVAYTFRITNNSIYSRLKVSSEGF 268
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                                                                                                                                                                                                                                                                                    3 OKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-MAR-2003 (IrEMBLrel. 23, Created)
01-MAR-2003 (IrEMBLrel. 23, Last sequence update)
01-MAR-2003 (IrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).

EMBL: D82205; BAA21939.1: -
InterPro: IPR001480; B_lectin.
InterPro: IPR003699; Pan_app.
InterPro: IPR003699; Slocus_glycop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                     428 AA
                                                                                                                                                                                                                                                            10; Mismatches
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                                                                                                                                                                                                                                     Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01453; Agglutinin; 1.
Pfam; PF00954; S.locus_glycop; 1.
SMART; SM00108; B_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                 S-locus glycoprotein (Fragment).
                                                                                                                                                                                                                                     32.5%;
25.6%;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.6%
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein (Fragment)
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                                                                                                                                                                                                     430
                                                          Brassica napus (Rape).
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                                                                                                     NCBI_TaxID=3708;
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SEQUENCE
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023839
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGURANCE ANOLY.

A MAINE-ATCC35047;

A Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;

A Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;

A Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;

A Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;

B Manuta Manuta H. Andrabasa M. Andrabases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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                                                                                                                                                                                                                                                                                                                                                  dsDNA viruses, no RNA stage; Papillomaviridae;
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Last annotation update)
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Last annotation update)
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507 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AVRLYHYEDKEKNNIAKFKRFLPLG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AHQIYQFTDKDKDNVAPRSKISPQG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 240:359-365(1998).
EXBL; Y1576; CAA75476.1; .
InterPro: IPR002210; PV_capsid_Ll.
Pfam; PP00500; late_protein_Ll; 1.
PRINTS; PR00865; HPVCAPSIDLI.
PRODM; PD0000544; PV_capsid_Ll; 1.
SEQUENCE 507 AA; 56998 MW; 6F1758
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                                                                                                                                                                                                                  E7, E1, E2, E4, L2, and L1 genes
                                                                                      Created)
    PRT;
                                                                                                                                                                                                                                                                                                         Human papillomavirus type 80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.9%;
38.2%;
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                                                                                  (TrEMBLrel. 06, (TrEMBLrel. 06, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=29323;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=69987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          αd
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Search completed: October 14, 2003, 08:40:19 Job time: 44.5682 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 08:37:31; Search time 20.4318 Seconds

(without alignments)
64.196 Million cell updates/sec

Title: US-09-931-700-3

Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNNAPRSKISPQGY 31
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

328717 seqs, 42310858 residues

Searched:

328717

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued_Patents_AA:*
1: \cgn2_c/ptodata/1/iaa/5A_COMB.pep:*
2: \cgn2_c/ptodata/1/iaa/5B_COMB.pep:*
3: \cgn2_c/ptodata/1/iaa/6A_COMB.pep:*
4: \cgn2_c/ptodata/1/iaa/6B_COMB.pep:*
5: \cgn2_c/ptodata/1/iaa/6B_COMB.pep:*
6: \cgn2_c/ptodata/1/iaa/6B_COMB.pep:*
6: \cgn2_c/ptodata/1/iaa/bec/files1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 23, Appl	3	Sequence 14, Appl	σì	9	11,	14,	ŕ	'n	H	H	Sequence 5, Appli	ě	a,	'n	3,	4	æ	7,	ě	15	'n	H	17,	16,	15	
SUMMAKIES	DI	-070-	US-09-011-922A-3	-09-011-	9	-09-280-501-	US-09-280-501-11	õ	-06	õ	US-08-486-596A-1	ö	US-09-280-501-5	US-08-233-389C-3	US-08-801-863-3	US-08-486-596A-3	US-09-004-713-3	US-09-280-501-4	US-09-280-501-8	US-09-280-501-7	US-09-280-501-3	US-09-070-504-15	US-09-280-501-2	US-09-280-501-1	-09-280-501	-501	-280-501	US-09-280-501-10
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ď	Query Match Length DB								-	_	100.0			•													45.4	
	Score 1								163				158	157	157	157	157	154	150	150	149	148	144	140	123	112	74	89
	Result No.	H	7	3	4	2	9	7	89	5	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 24655, A Sequence 17, Appl Sequence 17, Appl
US-09-011-922A-2 US-08-966-38B-4 US-09-18B-403-4 US-09-281-259-4 US-09-252-991A-24655 US-08-934-402-17 US-09-207-621-17 US-09-207-621-17 US-09-33-402-17 US-09-33-417-17 US-09-33-421-17 US-08-934-224-17 US-08-934-224-17 US-08-934-224-17 US-08-934-224-17 US-08-934-224-17 US-08-934-224-17 US-08-934-224-17 US-08-934-224-17 US-08-934-223-17 US-08-934-223-17 US-08-280-201-14 US-09-786-240-31
40000400000000000
13 775 775 775 775 1005 100 100 100 100 100 100 100 100 1
23.00 20.00
52 52 52 53 53 53 53 53 53 54 54 54 54 54 54 54 54 54 54 54 54 54

ALIGNMENTS

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Gaps
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                                                                                                                                                      TITLE OF INVENTION: PERTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 163; DB 3;
100.0%; Pred. No. 2.4e-19;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                       ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CILASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, Myra H
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 Sequence 23, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION
APPLICANT: Saha, Shankar
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 612/305-1220
612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                             55401
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RESULT 1
US-09-070-504-23
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COUNTRY:
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                                                                                                                                                                                            Functional Role of Adrenomedullin (AM) and the Gene-Related Product (PAMP) in Human Pathology and Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 163; DB 4; Length 31; 100.0%; Pred. No. 2.4e-19; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                      APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen: Macri, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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APPLICATION NUMBER: US/60/002,514
FILING DATE: 18 Aug-1995
FILING DATE: 18 Aug-1995
FILING DATE: 30-Aug-1995
FILING DATE: 30-Aug-1995
FILING DATE: 30-Aug-1995
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
FILING DATE: 12-Mar-1996
FILING DATE: 12-Mar-1996
FILING DATE: 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REDABLE FORM:
MEDIUM TYBE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Peb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                        E: MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
                                           Sequence 3, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,335
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEFONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 amino acids
                                                                                                                                                                                       TITLE OF INVENTION: FUNC
TITLE OF INVENTION: Adre
TITLE OF INVENTION: Pro
TITLE OF INVENTION: Phys
NUMBER OF SEQUENCES: 17
CCRRESPONDENCE ADDRESS:
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                                                                                   GENERAL INFORMATION:
APPLICANT: CUTTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                   10154-0053
                                                                                                                                                                                                                                                                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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STREET: 34
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RESULT 2
US-09-011-922A-3
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                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
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RESULT 3 US-09-011-922A-14

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                                                           APPLICANT: Cuttifta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo; Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 163; DB 4; Length 31; 100.0%; Pred. No. 2.4e-19; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic homolog of two-thirds of the intact AM peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: US/60/013,172
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2026-4202US3
                                                                                                                                                                                                                                                                                                     MORGAN & FINNEGAN, L.L.P.
Sequence 14, Application US/09011922A Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cooper, Garth James Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/09280501; Patent No. 6440421; GENERAL INFORMATION: APPLICANT: Cooper, Garth James Smit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leslie A. Serunian
                                                                                                                                                                                                                                                                                                                           345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO FEATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                  RY: USA
10154-0053
                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      STREET: 345 FORTY: New York
                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                          ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-280-501-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 3-CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-233-389C-1
                                                                                                                                                                                                                                                                                                                                                                                       US-09-070-504-14
                                                                                                                                   US-09-280-501-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                    LENGTH: 40
                                                                                           TYPE: PRT
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Jillian
APPLICANT: Cornish, Jillian
IIILE OF INVENTION: TREATHENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 0897-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR PILING DATE: 1996-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-280-501-6
Sequence 6, Application US/09280501
Patent No. 6440421
SPATENT INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: ADBRONGEDULLIN OR ADBRONGEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
    APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN ACONISTS
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT APPLICATION NUMBER: US/09/280,501
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NGS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 163; DB 4; Length 38; 100.0%; Pred. No. 3.1e-19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
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Best Local Similarity 100. Matches 31; Conservative
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US-09-280-501-9
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US-09-280-501-11
                                                                                                                                                                                                                                           SEQ ID NO 9
LENGTH: 31
TYPE: PRT
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LENGTH: 38
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                                                         ch 100.0%; Score 163; DB 4; Length 40; I Similarity 100.0%; Pred. No. 3.3e-19; 31; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , DB 3;
4.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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                                                                                                                                                        1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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100.0%; Pred. No. 4.5
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                              ; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MCCormack, Myra H
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Derek D. APPLICANT: Saha, Shankar APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 612/305-122
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 31; Conservative
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ORGANISM: Homo sapiens
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Length 185;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
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100.0%; Score 163; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 31; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.1e-18;
tive 0; Mismatches 0;
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                                                                          NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SEGN-5 DIV3
TELECOMMUNICATION INPORMATION:
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NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
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ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/486,596A FILING DATE: JUNE 7, 1995 CLASSIFICATION: 530
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APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08486596A; Patent No. 5837823
                                                                                                                                                                                               TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 100.vv,
-nbos 31; Conservative
                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
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TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1
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LENGTH: 185 amino acids
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; MOLECULE TYPE: protein
US-08-801-863-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-486-596A-1
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                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
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                                                                                                                    APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: c/o FISH & NEAVE
1251 Avenue of the Americas
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Fatent No. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KATAMURA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MATSUO, Hisayuki
TITLE OF INVENTION: ADRENOMEDULIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                             KITAMURA, Kazuo
KANGAWA, Kenji
MATSUO, Hisayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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GENERAL INFORMATION:
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                                                                                       APPLICANT:
APPLICANT:
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                                                                               Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                             96.9%; Score 158; DB 4; I
100.0%; Pred. No. 1.5e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                          1 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 30
                                                                                                                                                                 2 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KTANURA, Kazuo
APPLICANT: KTANURA, Kenji
APPLICANT: MATSOO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDERE ADDRESS:
ADDRESSED: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/233,389C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08233389C; Patent No. 5639855; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08801863 Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSOO, Hisayuki
APPLICANT: ETO, Tanenao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: 27,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                         30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: protein US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 26-APF
CLASSIFICATION: 530
                   ORGANISM: Homo sapiens
                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                             US-08-233-389C-3
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US-08-801-863-3
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                                       US-09-280-501-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                               Query Match
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APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADDENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: U8/09/280,501
CURRENT APPLICATION NUMBER: 08/634,562
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk Compatible Compatible Compatible Compatible Corresponding System: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713 FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVZ CON TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 163; DB 2;
100.0%; Pred. No. 2.1e-18;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TVQKLAHQIXQFTDKDKNAPRSKISPQGY 146
116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
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                                                                                                                                                                                                                                                                                                                 E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
TITLE OF INVANTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09280501
Patent No. 6440421
                                                                                                     Sequence 1, Application US/09004713 Patent No. 5910416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INPORATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 185 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                        USA
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US-09-280-501-5
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US-09-004-713-1
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                                                                                                    COMPUTER READBLE FORM:
MEDUJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAMM: HALLEY Jr., James F.
REGISTRAION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPRA: (212) 596-9000
TELEBRA: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENTH: 188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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APPLICANT: KITAMORA, Kazuo
APPLICANT: KANCAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/08486596A; Patent No. 5837823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 30; Conserva
             STREET: 1202 ...
                                                                                  USA
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                                                            STATE: NO COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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96.3%; Score 157; DB 2; Length 188; 96.8%; Pred. No. 2e-17; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                        1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 14, 2003, 08:41:22
                       TELEPHONE: (212) 596-9000
TELERAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRRACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-596A-3
           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                Query Match
Best Local Similarity 96.8%
                                                                                                                                                                                                                                                                                                                                                                                                  Job time : 21.4318 secs
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                                                                                                                                                                                                                                                                                                                       g
TITLE OF INVENTION: ADRENOMEDULLIN NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 14, 2003, 08:40:27; Search time 62 Seconds (without alignments) 80.564 Million cell updates/sec Run on:

US-09-931-700-3 Perfect score:

163 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

600653 seqs, 161128416 residues Searched:

600653 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 3, Appli	Sequence 14. Appl	Sequence 23, Appl	Sequence 14. Appl	`~		4	Sequence 31 Appl	Sequence 4. Appli	Sequence 3547, Ap	Sequence 8547, Ap	Sequence 43882, A	Sequence 570, App	Sequence 174. App	Sequence 41, Appl
	ID	US-09-931-700-3	US-09-931-700-14	US-09-813-345-23	US-09-813-345-14	US-10-197-954-2	US-09-813-345-15	US-09-931-700-2	US-10-427-631-31	US-09-795-061-4	US-10-128-714-3547	US-10-128-714-8547	US-09-864-761-43882	US-10-102-806-570	US-09-903-190-174	US-09-738-269-41
		. 6	6	σ	9	15	σ	σ	12	12	15	15	OJ.	15	12	12
	Query Match Length DB	31	31	31	52	52	20	13	478	1745	984	1058	33	327	131	608
æ	Query	100.0	100.0	100.0	100.0	100.0	8.06	35.0	29.4	29.4	29.1	29.1	28.8	28.8	28.5	28.2
	Score	163	163	163	163	163	148	57	48	48	47.5	47.5	47	47	46.5	46
	Result No.	-	7	m	4	2	9	7	80	6	10	11	12	13	14	15

401001 - H H H H H H H H H H H H H H H H H H	Sequence 74, Appl Sequence 74, Appl Sequence 74, Appl Sequence 74, Appl Sequence 74, Appl
1 US-10-023-437 2 US-10-269-191-279 2 US-10-352-3933 2 US-10-352-3933 2 US-10-352-3933 2 US-10-352-3933 2 US-10-441-667 2 US-10-441-667 2 US-10-441-667 2 US-10-441-667 2 US-10-441-667 2 US-10-441-667 2 US-10-18-18-18-18-18-18-18-18-18-18-18-18-18-	12 US-10-219-225-/4 12 US-10-219-526-74 12 US-10-219-530-74 12 US-10-219-531-74 12 US-10-219-532-74
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11111202222222222222222222222222222222	* 4 4 4 4 1 4 6 4 5

ALIGNMENTS

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Sequence 3, Application US/09931700

Patent No. US20020055615A1

GENERAL INFORMATION:
APPLICANT: UTTITTA, FRANK
APPLICANT: MILLER, MAE JEAN
APPLICANT: MILLIAM
APPLICANT: WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202044
CURRENT APPLICATION NUMBER: US/09/931,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072, OTHER INFORMATION: PreproAM (amino acids 116-146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRENT FILING DATE: 2010-09-16
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR PILING DATE: 1998-02-17
PRIOR PLING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-16
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-31
PRIOR FILING DATE: 1995-08-31
SOFTWARE: PATENTING DATE: 3995-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
US-09-931-700-3
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APPLICANT: MILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KARLES
APPLICANT: MACRI, CHARLES
APPLICANT: MACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Physicial Research Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physical Product (PAMP) in Human Pathology and
                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE
                                                  Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 163; DB 9; Length 31; 100.0%; Pred. No. 3.2e-17; tive 0; Mismatches 0; Indels
                                                                                         Indels
                                             Score 163; DB 9;
Pred. No. 3.2e-17;
                    100.0%; Score
100.0%; Pred. No. 3.7.
0; Mismatches
                                                                                                                                                           1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 2001-08-16
PRIOR PILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/012,936
PRIOR APPLICATION NUMBER: US/60/002,936
PRIOR APPLICATION NUMBER: US/60/002,514
PRIOR PILING DATE: 1995-08-16
PRIOR PELING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/09813345
Patent No. US20020068814A1
GENERAL INFORMATION:
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Patent No. US20020055615A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smith, Derek D. Saha, Shankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                      Query Match
Best Local Similarity 100.0
Matches 31; Conservative
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es 31; Conserv
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APPLICANT: CUTTITA
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US-09-931-700-14
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US-09-931-700-3
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31;
STREET: 119 No. US20020068814Alth Fourth Street CITY: Minneapolis
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ADDRESSEE: Mucting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814Alth Fourth Street
CITY: Minneapolis
                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 3.2e-17;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                NAME: MCCOIMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 180.00020101
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09813345
Patent No. US20020068814A1
GENERAL INFORMATION:
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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Saha, Shankar
Abel, Peter W.
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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Best Local Similarity 100.0
                                                                                                       USA
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                                                                                STATE: MN COUNTRY: U
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GENERAL INFORMATION:
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APPLICANT: Siddigi, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24743-2308
CURRENT APPLICATION NUMBER: US/10/197,954
CURRENT APPLICATION NUMBER: G0/366,019
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-11
SOFTWARE: FEASTER OF Windows Version 4.0
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Saha, Shankar
Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANNAGONISTS OF CGRP-RECEPTOR
SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 52;
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ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814Alth Fourth Street
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100.0%; Pred. No. 5.8e-17;
clve 0; Mismatches 0;
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                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 14:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
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Patent No. US20020068814A1
GENERAL INFORMATION:
                                 INFORMATION FOR SEQ 12.705-12.8

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERSTICS:
ENGINE SEQ amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10197954 Publication No. US20030119021A1 GENERAL INFORMATION:
                                                                                                                                                         STRANDEDNESS: single
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Best Local Similarity 100.
Matches 31; Conservative
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US-10-197-954-2
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LENGIH: 52
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                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MCGOrmack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1228
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/813,345 FILING DATE: 20-Mar-2001
                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                  FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS
                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.13
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                   COUNTRY: USA
ZIP: 55401
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Sequence 2, Application US/09931700 Patent No. US20020055615A1
                                                                                 APPLICANT: CUTTITIA, FRANK
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APPLICANT: GUTILITE, ALFREDO
APPLICANT: GUTILITE, ALFREDO
APPLICANT: MARTINEZ, ALFREDO
APPLICANT: MILLER, MAG JEAN
APPLICANT: MILLER, MAG JEAN
APPLICANT: MILLER, MILLIAM
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOWAS
APPLICANT: WALSH, THOWAS
APPLICANT: MACRI, CHARLES
APPLICANT: MACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202084
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-03-10
PRIOR FILING DATE: 1996-03-10
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18 NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin Ver. 2.1

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LENGIH: 1745
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29.4%; Score 48; DB 12; Length 478;
Best Local Similarity 24.5%; Pred. No. 81;
Matches 12; Conservative 7; Mismatches 12; Indels 18;
                                        OTHER INFORMATION: Description of Artificial Sequence: Peptide, OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TVQKLAHQIYQFTD-------KDKDNVAPRSKISPQGY 31
                                                                                                                                             Length 13;
                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: GenBank ID No. US20030175923A1 g2443814
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Publication No. US20030166842A1

GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Imamura, Yasutada
TITLE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
FILE REFRERNCE: 960296.96781

CURRENT APPLICATION NUMBER: US/09/795,061

CURRENT FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: INCYTE CORPORATION; TANG, Y. TOM;
APPLICANT: INCYTE CORPORATION; TANG, Y. TOM;
APPLICANT: CORLEY, Neil C.; GUGGLER, Karl J.;
APPLICANT: BAGGHN, Mariah R.; LaL, Preeti G.;
APPLICANT: YUE, Henry: HILLMAN, Jennifer L.;
APPLICANT: YEB, Henry: HILLMAN, Jennifer L.;
APPLICANT: AZIMZAI, Yald
TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
TITLE REPRENCE: PF-0592-1 DIV
CURRENT APPLICATION NUMBER: US/10/427, 631
CURRENT APPLICATION NUMBER: US/09/786,240
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR PLIING DATE: 1998-09-10
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-01-04
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGRAM
                                                                                                                                           DB 9;
0.06;
                                                                                                                                 Query Match
35.0%; Score 57; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/10427631
Publication No. US20030175923A1
GENERAL INFORMATION:
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     4 HQIYQFTDKD 13
                                                                                                                                                                                                                           7 HQIYQFIDKD 16
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US-10-427-631-31
                                                                                       US-09-931-700-2
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SOFTWARE: SEQ ID NO 4

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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Hu, Wengi
APPLICANT: Hu, Wengi
APPLICANT: Talshkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Landleux, Sebastien M
TITLE OF INVENTION: Methods of Use
FILE REPERRECE: 10182-018-999
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: US 60/395,899
PRIOR FILING DATE: US 60/395,899
PRIOR FILING DATE: US 60/395,899
PRIOR FILING DATE: US 60/316,362
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APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                            29.4%; Score 48; DB 12; Length 1745; 53.3%; Pred. No. 3.6e+02; Live 4; Mismatches 3; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%; Score 47.5; DB 15; 27.5%; Pred. No. 2.2e+02; tive 10; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                               Sequence 3547, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 8547, Application US/10128714; Publication No. US20030119013A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Aspergillus fumigatus US-10-128-714-3547
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223 DCDNLAPAATVAPQG 237
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3547
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                                                                            Query Match
Best Local Similarity 53.33
Matches 8; Conservative
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ORGANISM: Homo sapiens US-09-795-061-4
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Matches 11; Conserv
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US-10-128-714-3547
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Gaps
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN BARIA. = 0.94

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.00

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.00

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69

US-09-864-761-43882
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| Publication No. US20030054421A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REPERENCE: PALOSPICA
| CURRENT APPLICATION NUMBER: US/10/102,806
| CURRENT FILING DATE: 2002-03-22
| PRIOR APPLICATION NUMBER: 09/925,298
| PRIOR APPLICATION NUMBER: PCT/US00/05881
| PRIOR PILING DATE: 2000-03-08
| PRIOR PELING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 846
| COFTURED DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.8%; Score 47; DB 15; Length 327; 41.4%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.8%; Score 47; DB 9; Length 33; 62.5%; Pred. No. 5.3;
Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 43882
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APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TILLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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; Publication No. US20030162176A1
; GENERAL INFORMATION:
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Best Local Similarity 41.4%;
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Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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29.1%; Score 47.5; DB 15; Length 1058;
Best Local Similarity 27.5%; Pred. No. 2.4e+02;
Matches 11; Conservative 10; Mismatches 6; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QKLAHQIYQFTDK------DKDNVAPRSKISPQ 29
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Aspergillus fumigatus
US-10-128-714-8547
                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.1 SEQ ID NO 8547
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                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8603
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Sequence 41, Application US/09738269
Fublication No. US20030185848A1
GENERAL INFORMATION:
APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: STEME, CATHERINE
APPLICANT: STEME, CATHERINE
APPLICANT: STEME, CATHERINE
APPLICANT: MALTENBOECK, BERNHARD
TITLE OF INVENTION: MUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
TITLE OF INVENTION: CHLAMYDIA PSITTACI
FILE REFERENCE: UTSD:659
CURRENT APPLICATION NUMBER: US/09/738,269
CURRENT APPLICATION NUMBER: 2000-12-18
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                  PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: BARLIER APPLICATION NUMBER: 60/074,121
PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: BARLIER FILING DATE: 1998-08-10
PRIOR FILING DATE: BARLIER FILING DATE: 1998-10-04
SOFTWARE: PALENT.PM
SEQ ID NOS: 182
LENGTH: 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
28.5%; Score 46.5; DB 12; Length 131;
Best Local Similarity 33.3%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 8; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 28.2%; Score 46; DB 12; Length 608; Best Local Similarity 64.3%; Pred. No. 2.1e+02; Matches 9; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE

LOCATION: 40.41,43,60,70,76,82,86,105,107

CTHER INFORMATION: Xaa = any one of the twenty amino acids

US-09-903-110-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VQKLAHQ----IYQFTDKDKDNVAPRSKISPQGY 31
CURRENT APPLICATION NUMBER: US/09/903,190 CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Chlamydia psittaci
US-09-738-269-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 DKDNVAPRSKISPQ 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SIGNAL LOCATION: -20..-1 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-738-269-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 41
LENGTH: 608
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Search completed: October 14, 2003, 08:53:17

Job time : 63 secs

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

Sequence 2, Appli Sequence 935, App Sequence 935, App Sequence 14, Appli Sequence 74, Appli Sequence 63615, A Sequence 63615, A Sequence 12481, A

Sequence 14, Appl Sequence 6, Appli Sequence 11, Appl

Sequence

Seguence Sequence Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 148, App Sequence 12482, A Sequence 12482, A

Sequence 148, App Sequence 406, App Sequence 5, Appli

Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli

Sequence 3

Sequence

Sequence 7

Sequence Sequence

Sequence

Appli Appli 5, Appli

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US-09-623-548A-938

US-09-913-345-23

US-09-931-700-14

US-09-931-700-14

US-09-931-700-14

US-08-634-562-11

PCT-08-634-562-11

PCT-08-634-562-11

PCT-08-634-562-11

US-09-657-276-935

US-09-724-676-83615

US-09-724-676A-63615

US-09-724-676A-63615

US-09-724-676A-63615

US-09-724-676A-63615

US-06-453-050-12481

US-09-484-738A-112483

US-06-466-412-12481
                                                                                                                                                                                                                                                                                                                            05.01.018.924.2

05.01.018.924.2

05.01.030.298.2

05.01.040.068.148

05.05.00.453.050.11482

05.00.466.412.12482

05.00.466.412.12482

05.00.466.412.12482

05.00.466.412.12482

05.00.469.456.412.12482

005.08.634.562.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-018-924-4
US-10-030-298-4
US-08-634-562-4
US-09-475-158A-31
US-08-634-562-8
US-08-634-562-3
US-08-634-562-3
US-08-634-562-3
US-08-634-562-3
US-08-634-562-3
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US-09-813-345-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08634562
GENERAL INFORMATION:
APPLICANT: COY, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
FILE OF INVENTION: TREATMENT OF BONE DISO:
TILLE OF INVENTION: WITH ADRENOMEDULLIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Fish & Richardson P.C.
225 Franklin Street
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337
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                         1000.00
1000.00
1000.00
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STREET: ZZZ
TMV: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                        100.0
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 Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                (without alignments)
69.629 Million cell updates/sec
                                                                                               October 14, 2003, 08:38:52; Search time 405.114 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                  Pending_Patents_AA_Main:*

(ggn2_6/ptodata/1/paa/US06_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/paa/US101_COMB.pep:*/cgn2_6/ptodata/1/paa/US102_COMB.pep:*/cgn2_6/ptodata/1/paa/US103_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ptodata/1/paa/US104_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                          163
1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 10 US-08-634-562-9
                                                                                                                                                                                                                                                                5728757 seqs, 909918778 residues
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                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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163

No. Result

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STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-813-345-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Ezin, Alan
APPLICANT: Ezin, Alan
APPLICANT: Hilbaudeau, Karen
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION TOWBER: 60/134,406
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR APPLICATION NUMBER: 60/153,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 163; DB 10;
100.0%; Pred. No. 1.3e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 163; DB 20; 100.0%; Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                           FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: TSSO, Y. ROCKY
REGISTRATION NUMBER: 34,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
APPLICATION NUMBER: US/08/634,562 FILING DATE: 18-APR-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 938, Application US/09623548A GENERAL INFORMATION:
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-670
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                               TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-634-562-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-623-548A-938
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LENGTH: 31
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RESULT 3

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APPLICANT: Milner, Peter
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TILE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION: COMPONENTS
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-010-18
PRIOR FILING DATE: 1999-10-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PATENTIN VEF. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-657-276-938
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Saha, Shankar
Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 31;
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: CURROWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 163; DB 20; 100.0%; Pred. No. 1.3e-17;
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REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TVQKLAHQIYQFTDKDKDKNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 119 North Fourth Street CITY: Minneapolis
Sequence 938, Application US/09657276 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09813345 GENERAL INFORMATION:
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                                     APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
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Query Match
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APPLICANT: MILLER, MAE JEAN
APPLICANT: MILLER, MAE JEAN
APPLICANT: MILLER, MAE JEAN
APPLICANT: WISWORTH, EDWARD J.
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, CHARLES
APPLICANT: MACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202US4
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                    Query Match 100.0%; Score 163; DB 23; Best Local Similarity 100.0%; Pred. No. 1.3e-17; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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CURRENT FILING DATE: 2001-08-16
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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% Sequence 14, Application US/09931700

; GENERAL INFORMATION:
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                                                               LENGTH: 31 amino acids
TELEFAX: 612/305-1228
                                                                                     TYPE: amino acid
STRANDEDNESS: single
              INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
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; APPLICANT: CUTTITTA, FRANK
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                                                                                                                                                                                                        US-09-813-345-23
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US-09-931-700-3
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          APPLICANT: MILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: HOSE, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KARENS
APPLICANT: GREY, KARENS
APPLICANT: MCRI, CHARLES
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Peptide, OTHER INFORMATION: Synthetic homolog of AM (P072), Structural an OTHER INFORMATION: acid sequence representing two-thirds of the OTHER INFORMATION: intact AM peptide
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GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Cooper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
TITLE OF INVENTION: WITH ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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SOFTWARE: FastSEQ for Windows Version 2.0b
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                                                                                                                                                                                                                                    HILLE REFERENCE: 2026 4202034
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR APPLICATION NUMBER: US/60/002,514
PRIOR FILING DATE: 1995-08-18
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APPLICATION NUMBER: US/08/634,562
FILING DATE: 18-APR-1996
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
MARTINEZ, ALFREDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 31
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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ZIP: 02110-2804
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31; Conservative
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US-09-623-548A-935
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PCT-US02-22821-2
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LENGIH: 52
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           Matches
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100.0%; Score 163; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 31; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: COY, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Cooper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
TITLE OF INVENTION: WITH ADRENOMEDULLIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 163; DB 10;
Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/634,562
FILING DATE: 18 - APR-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 38
                                     NAME: TSAO, Y. ROCKY
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 08987/002001
TELECOMMULICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFRONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08987/002001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08634562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34,053
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                              TELEX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-634-562-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER
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02110-2804
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APPLICANT: Siddigi, Suhalb
APPLICANT: Siddigi, Suhalb
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
FILE REFERENCE: 24743-2305
CURRENT APPLICATION NUMBER: PCT/US02/22821
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFFWARE: FastSEQ for Windows Version 4.0
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| Sequence 935, Application US/09623548R
| Sequence 935, Application US/09623548R
| APPLICANT: Codjudhem, Inc.
| APPLICANT: Milner, Peter
| APPLICANT: Milner, Peter
| APPLICANT: Holmes, Darren
| APPLICANT: Thibaudeau, Karen
| TITLE OF INVENTION: PROFECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
| TITLE OF INVENTION: COMPONENTS
| TITLE OF INVENTION OF SEPTIMENTS ACTIVITY THROUGH CONJUGATION TO BLOOD
| CURRENT APPLICATION NUMBER: US/09/623,548A
| PRICE APPLICATION NUMBER: 60/134,406
| PRICE APPLICATION NUMBER: 60/134,406
           Gaps
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; Pred. No. 2.5e-17;
0; Mismatches 0; Indels
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                                                                                     10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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0; Mismatches
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PRIOR PILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SEQ ID NO 935
                                                                                                                                                                                                                                             ; Sequence 2, Application PC/TUS0222821
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    APPLICANT: HK Pharmaceuticals, Inc.
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.0
Matches 31; Conservative
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us-09-931-700-3.rapm

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MEDIUM TYPE: Floppy disk
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LENGTH: 52
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APPLICANT: Conjuchem, Inc.
APPLICANT: Exin. Alan
APPLICANT: Exin. Alan
APPLICANT: Exin. Alan
APPLICANT: Hilber, Peter
APPLICANT: Hilber, Peter
APPLICANT: Thibaudeau, Karen
TILLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TILLE OF INVENTION: COMPONENTS
TILLE OF INVENTION WINDER: US/09/657,276
CURRENT APPLICATION NUMBER: US/09/657,276
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-10
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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                                                                                    Length 52;
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ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 North Fourth Street
                                                                              ; Score 163; DB 20;
; Pred. No. 2.5e-17;
0; Mismatches 0;
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100.0%; Pred. No. 2.5e-17;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
                                                                                100.0%;
100.0%;
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                                                                        Query Match 100.0
Best Local Similarity 100.0
Matches 31; Conservative
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Matches 31; Conservative
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COUNTRY: U
                                     US-09-623-548A-935
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US-09-657-276-935
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LENGTH: 52
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APPLICANT: K"ster, Hubert
APPLICANT: Siddigi, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24743-2305
CURRENT PILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/306,019
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220

TELEPHONE CHARACTERISTICS:

SEQUENCY CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Sequence 2, Application US/10197954 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 31; Conservative
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Matches 31; Conservative
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US-10-197-954-2
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GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornells J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DAIE: 2003-02-077
PRIOR APPLICATION NUMBER: EP 02077060.8
PRIOR APPLICATION NUMBER: EP 02077060.8
SOFTWARE: Patentin version 3.1
SEQ ID NO 74
LENGTH: 52
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129:1914 Compugen
CURRENT APPLICATION NUMBER: US,09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 9722
SOFTWARE: Patentin version 3.2
ED ID NO 63615
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 163; DB 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-724-676-63615; Sequence 63615, Application US/09724676; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT CRGANISM: Homo sapiens US-09-724-676-63615
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